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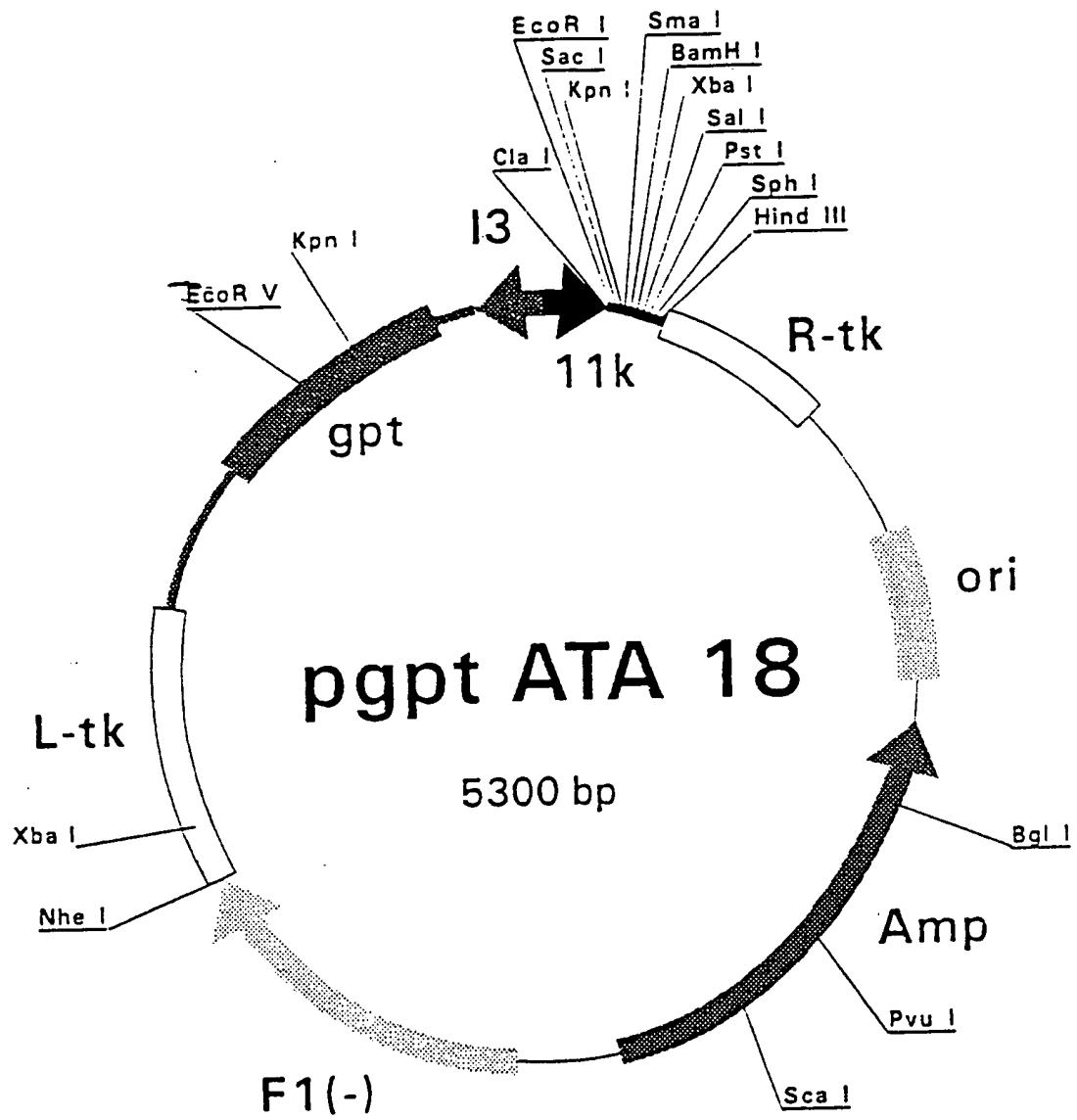


Fig. 1

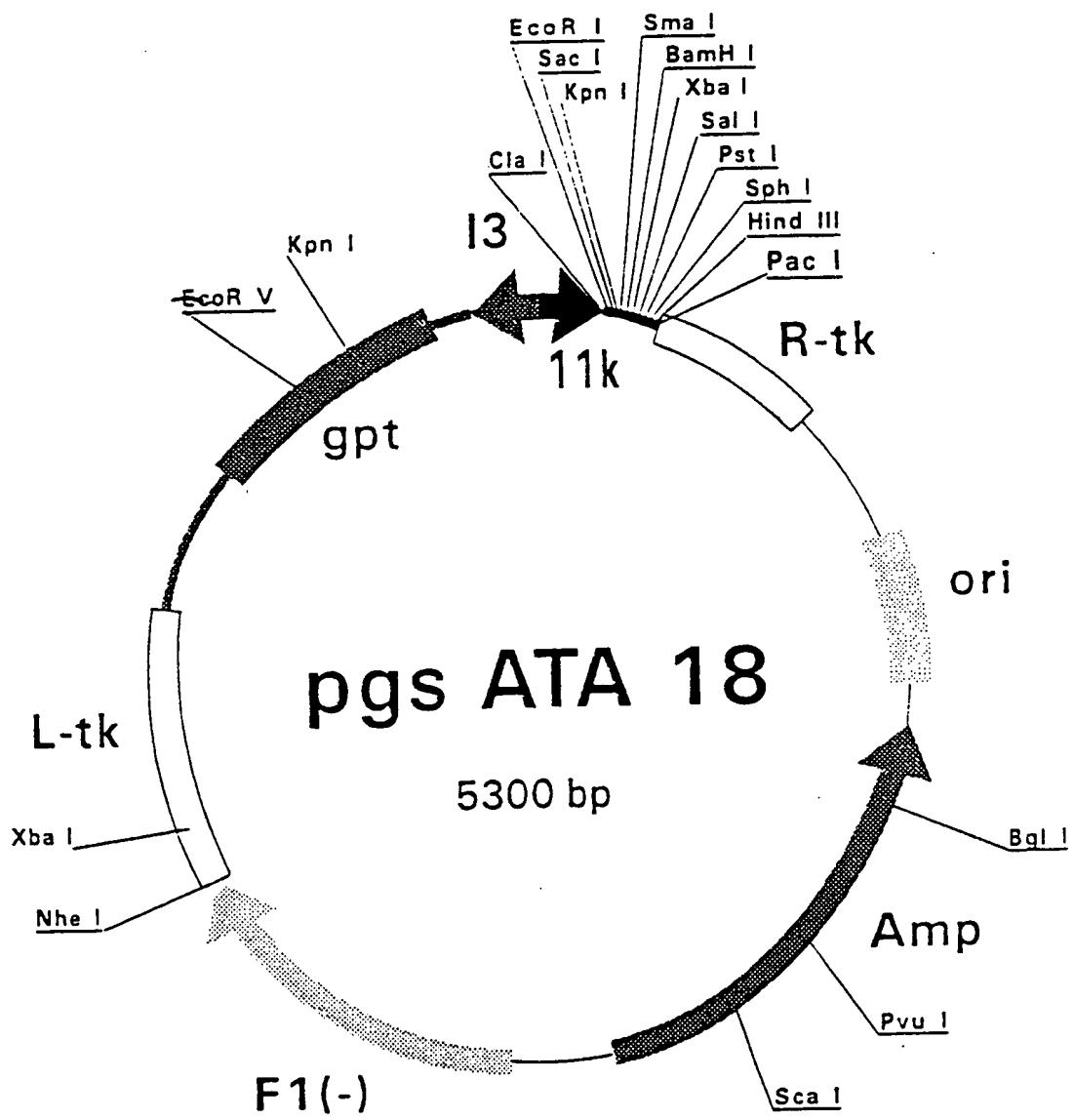


Fig. 2

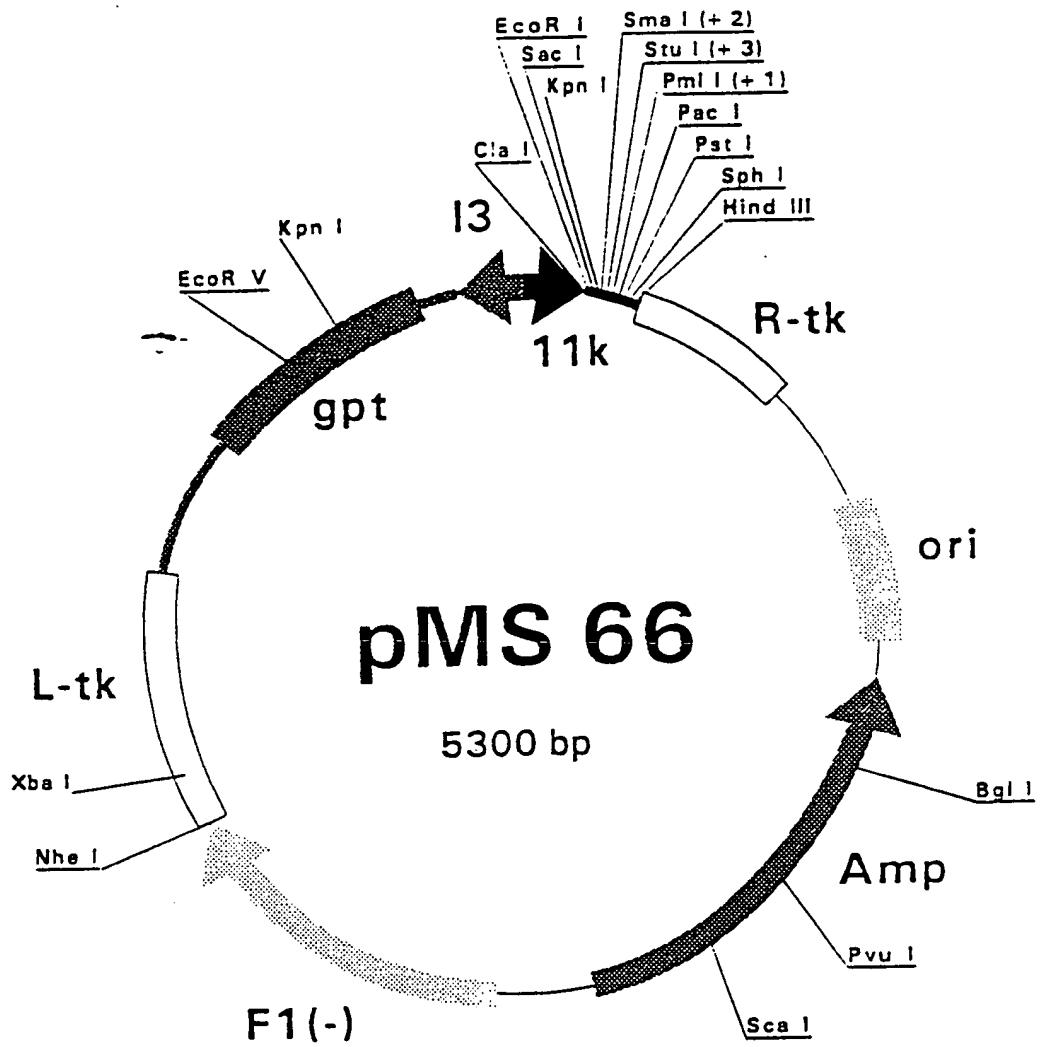


Fig. 3

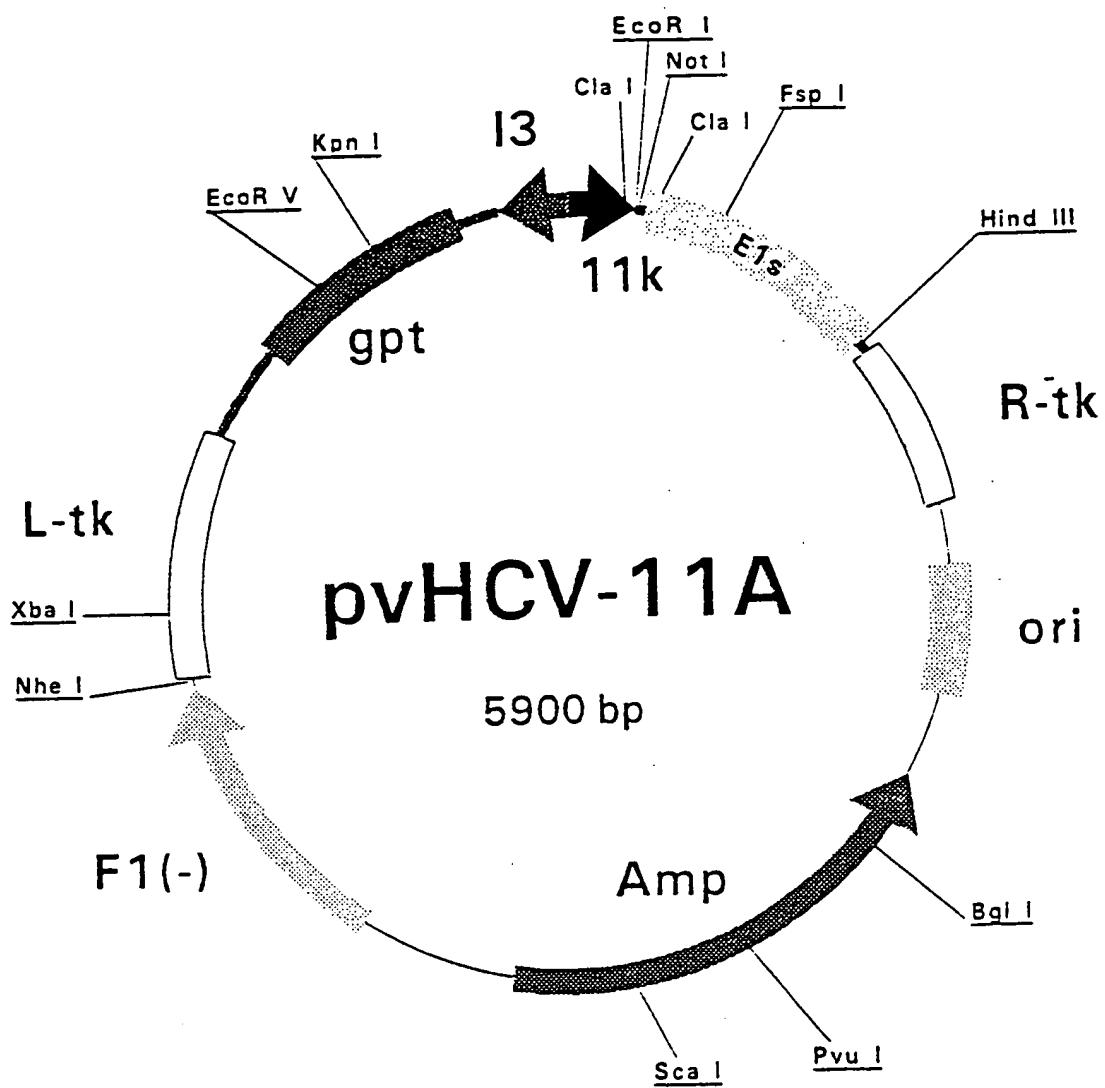
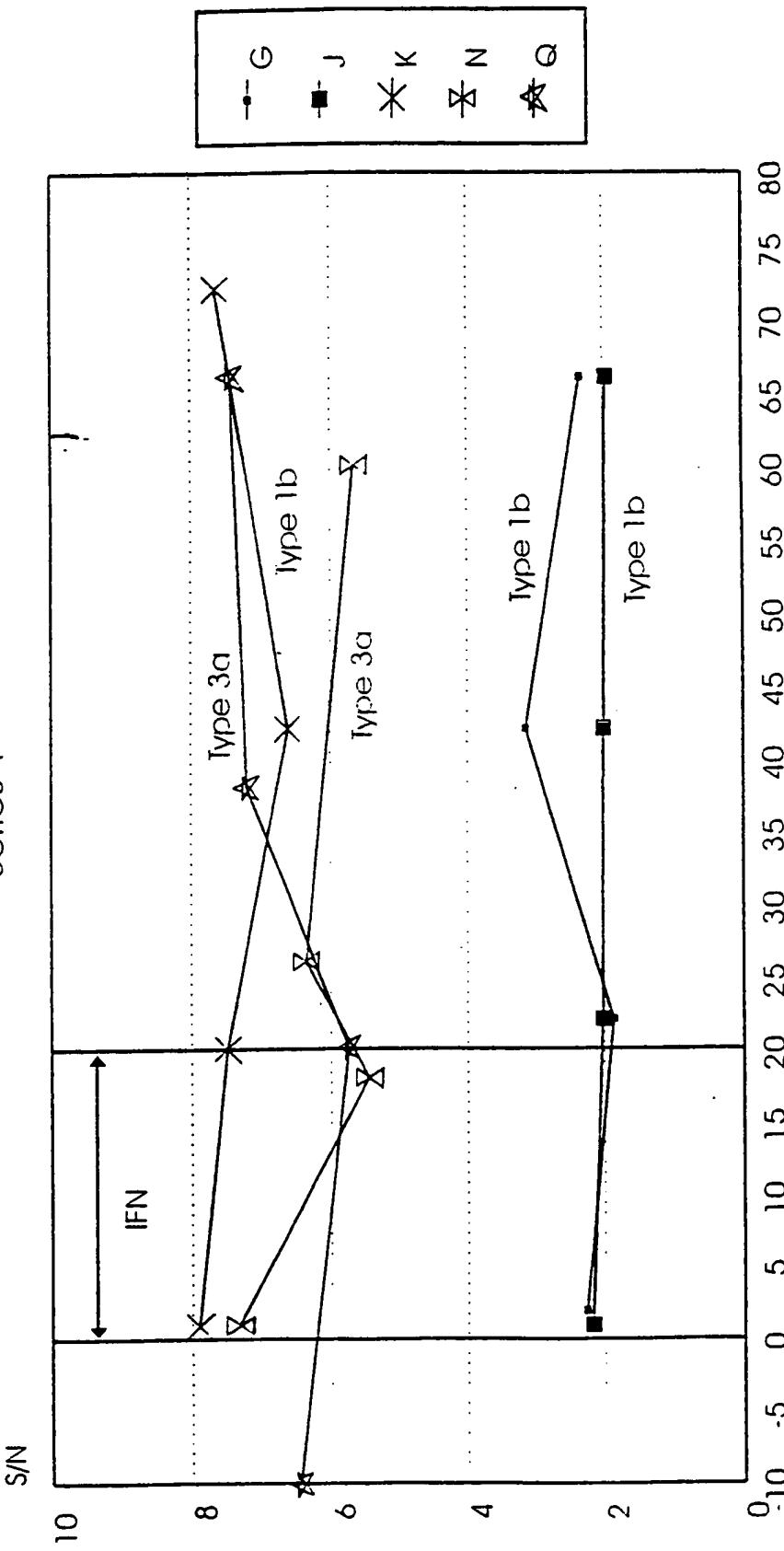


Fig. 4

# Anti-E1 levels in NON-responders to IFN treatment

Series 1

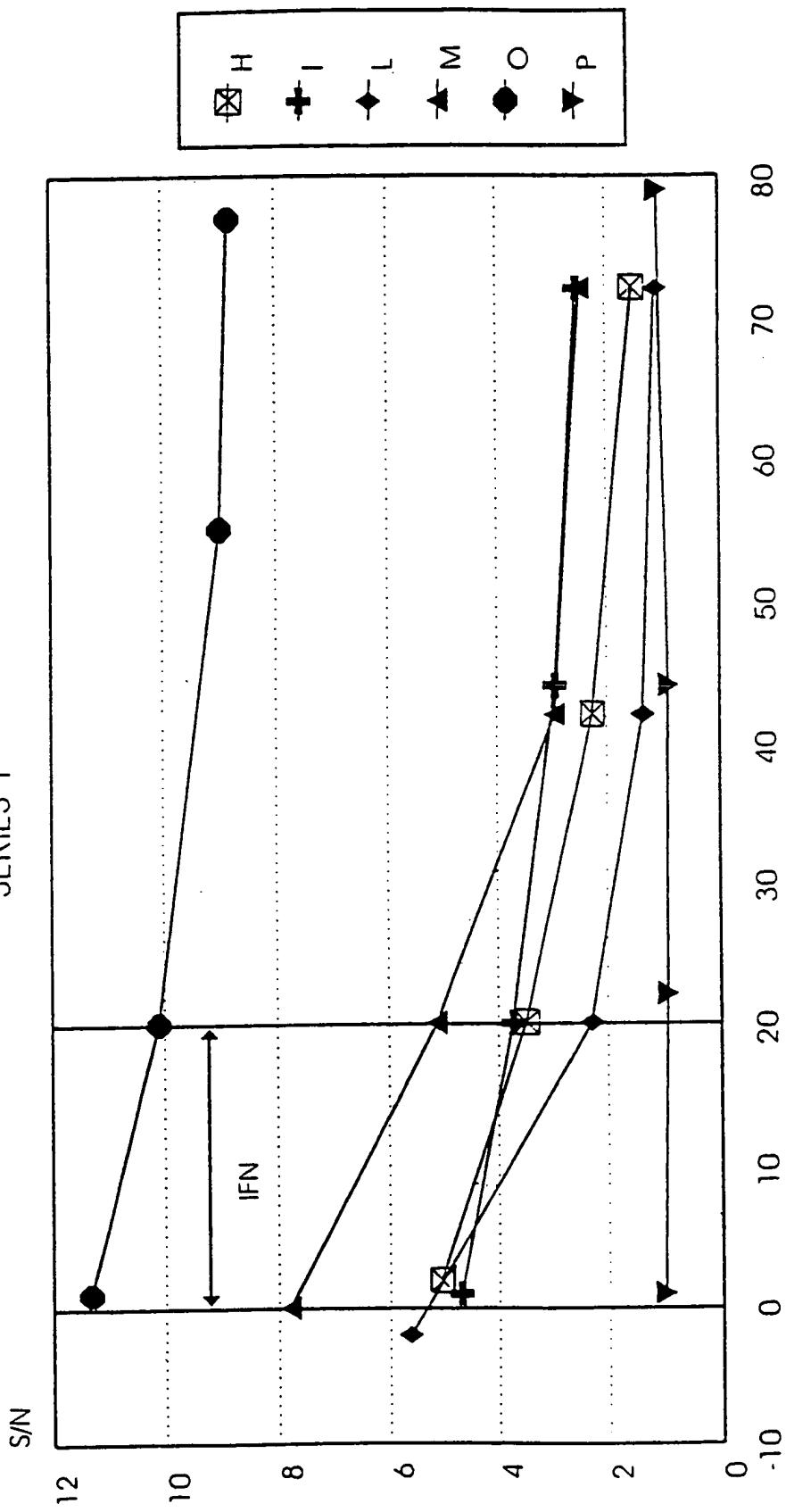


weeks after start of treatment

Fig. 5

Anti-E1 levels in RESPONDERS to IFN treatment

SERIES 1



weeks after start of treatment

Fig. 6

Anti-E1 levels in patients with COMPLETE response to IFN

SERIES 2

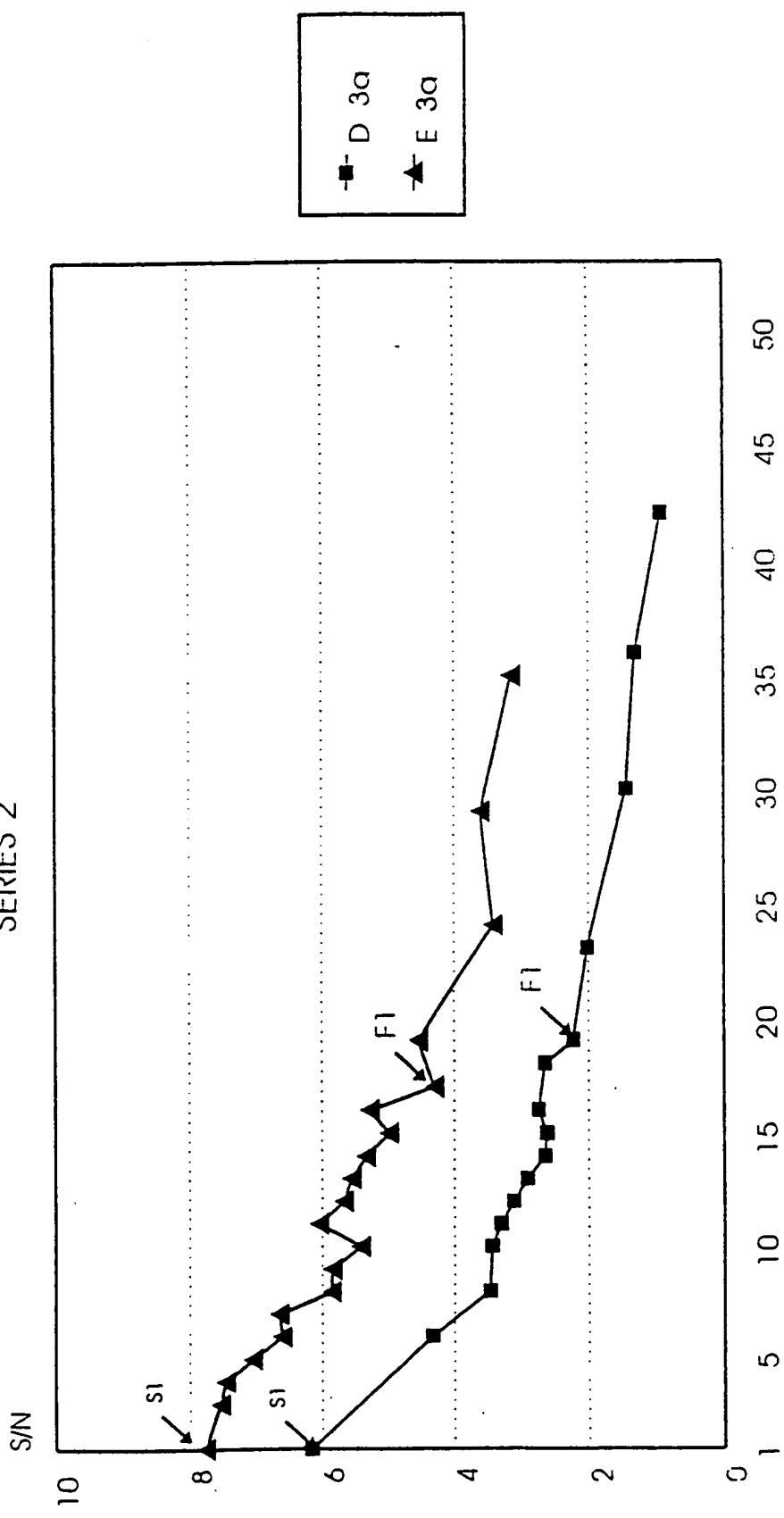
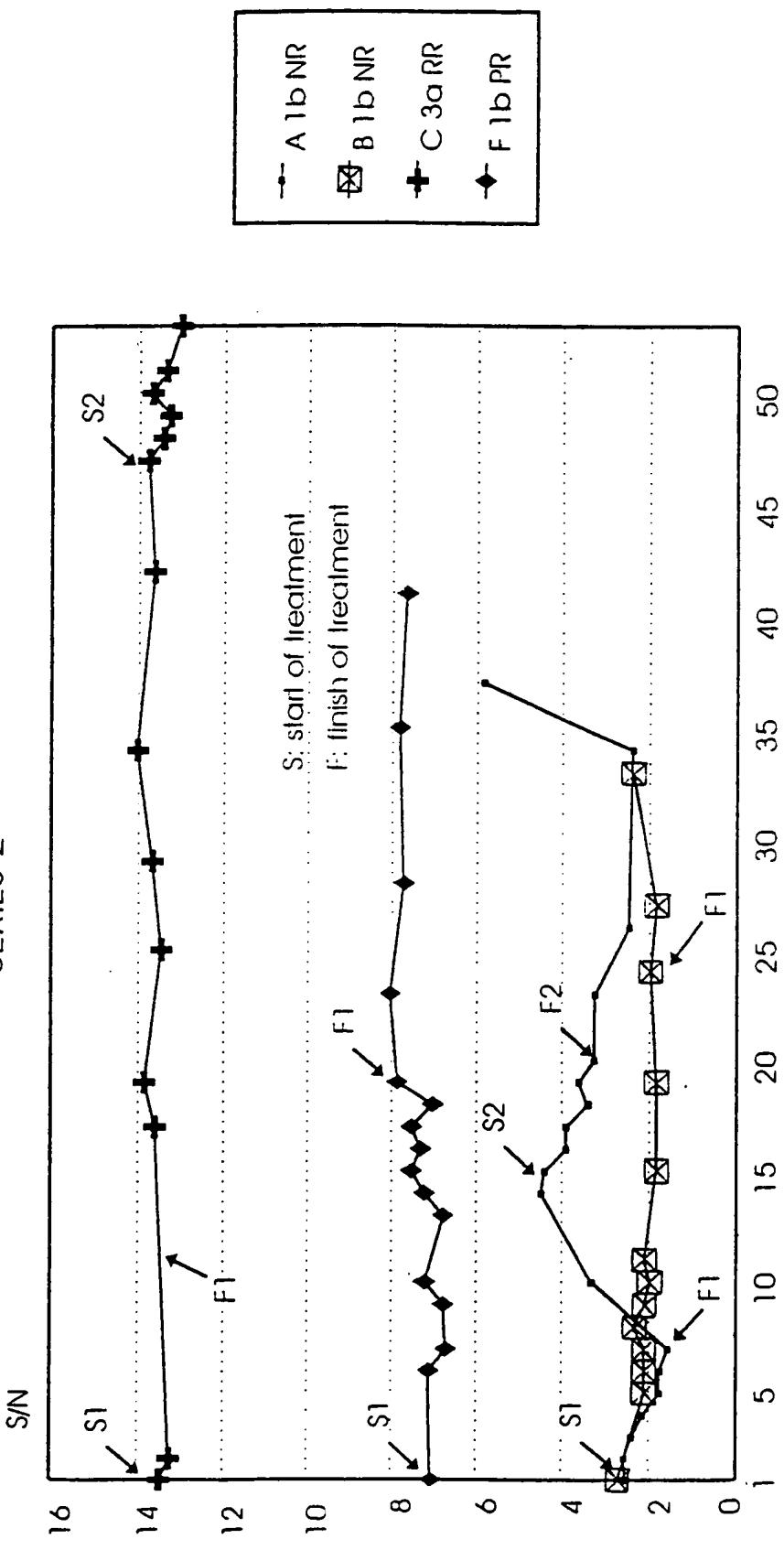


Fig. 7  
months after start of treatment

# Anti-E1 levels in INCOMPLETE responders to IFN treatment

## SERIES 2



months after start of treatment  
Fig. 8

# Anti-E2 levels in NON-RESPONDERS to IFN treatment

## SERIES 1

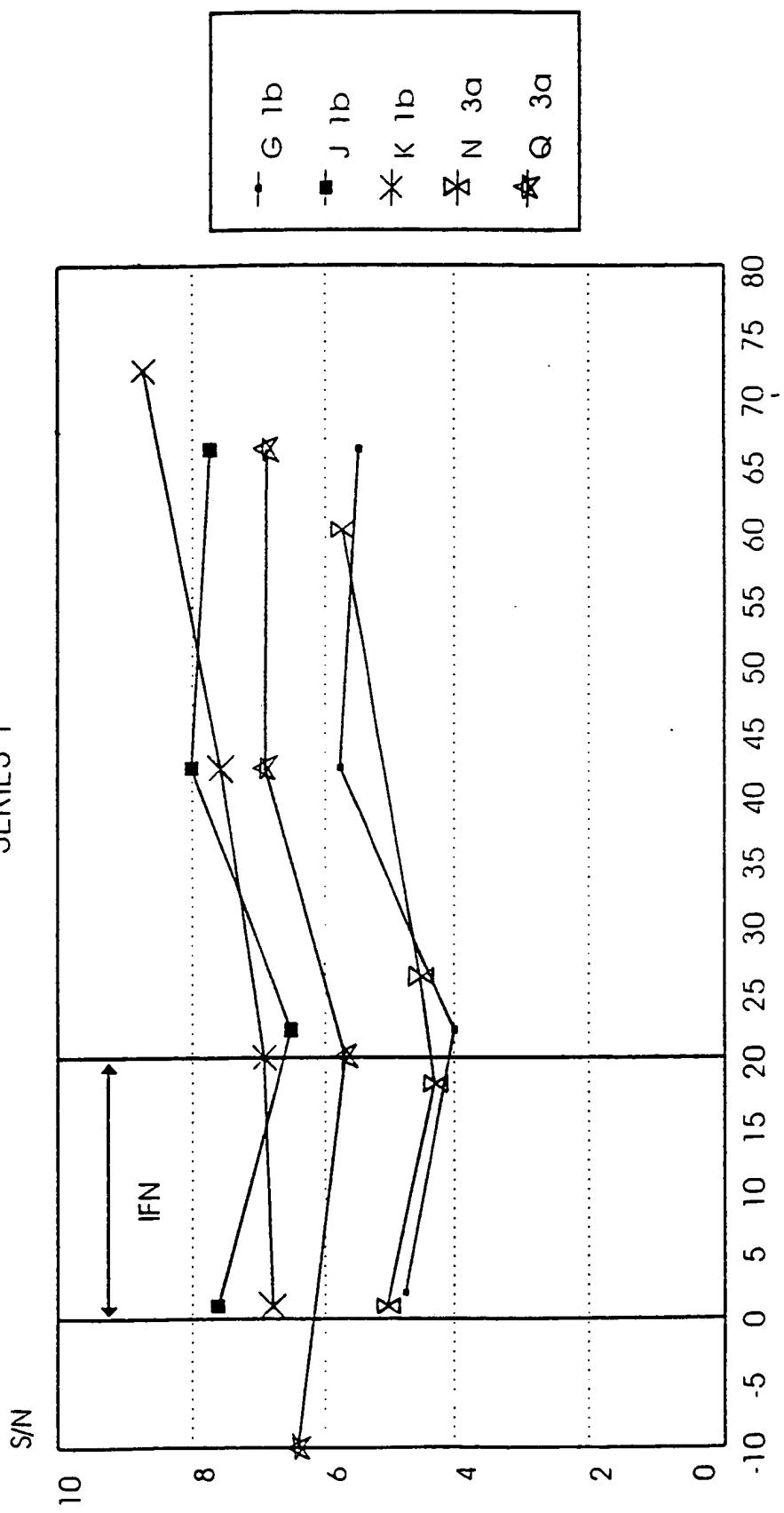
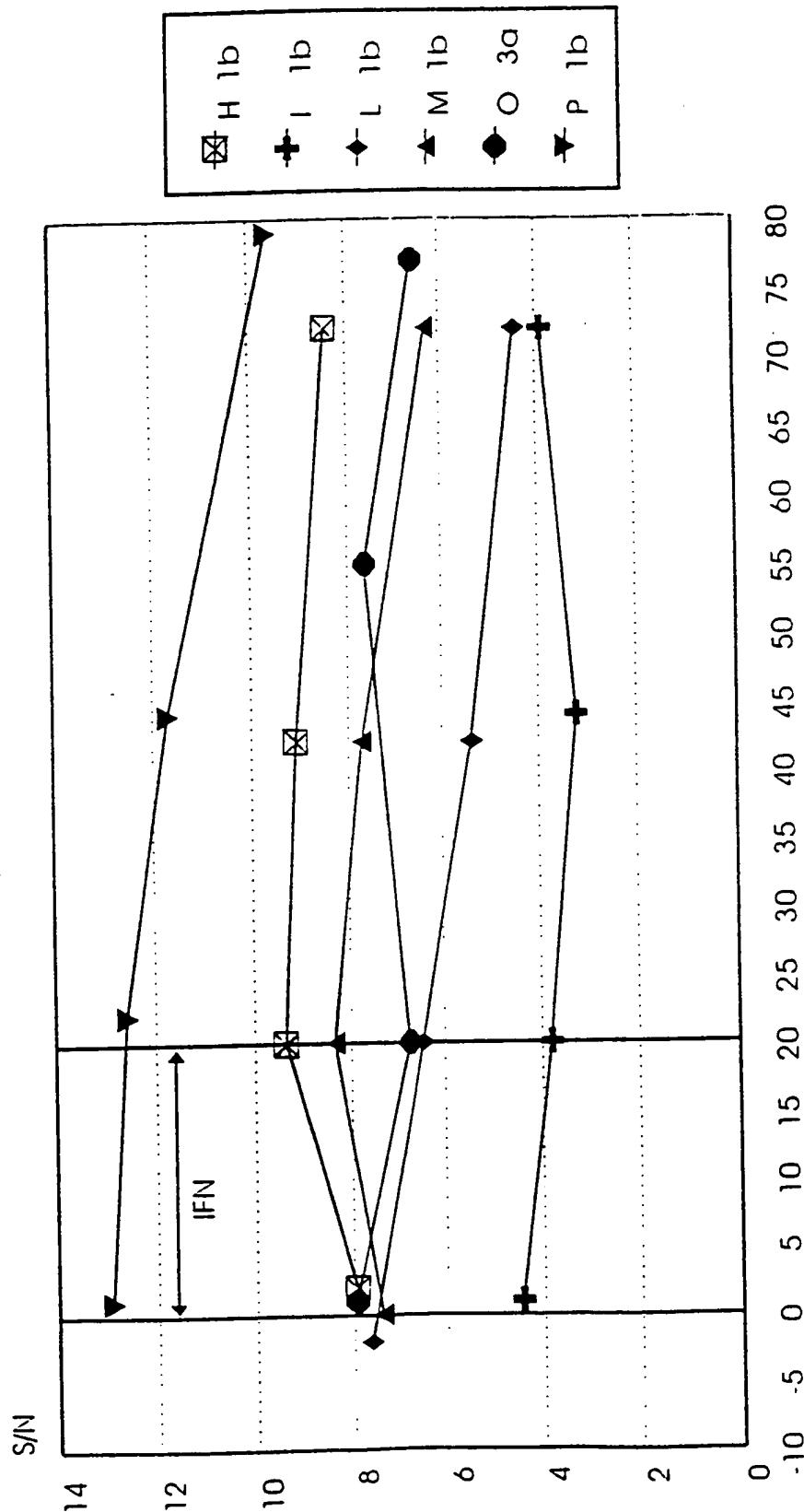


Fig. 9  
weeks after start of treatment

# Anti-E2 levels in RESPONDERS to IFN treatment

## SERIES 1

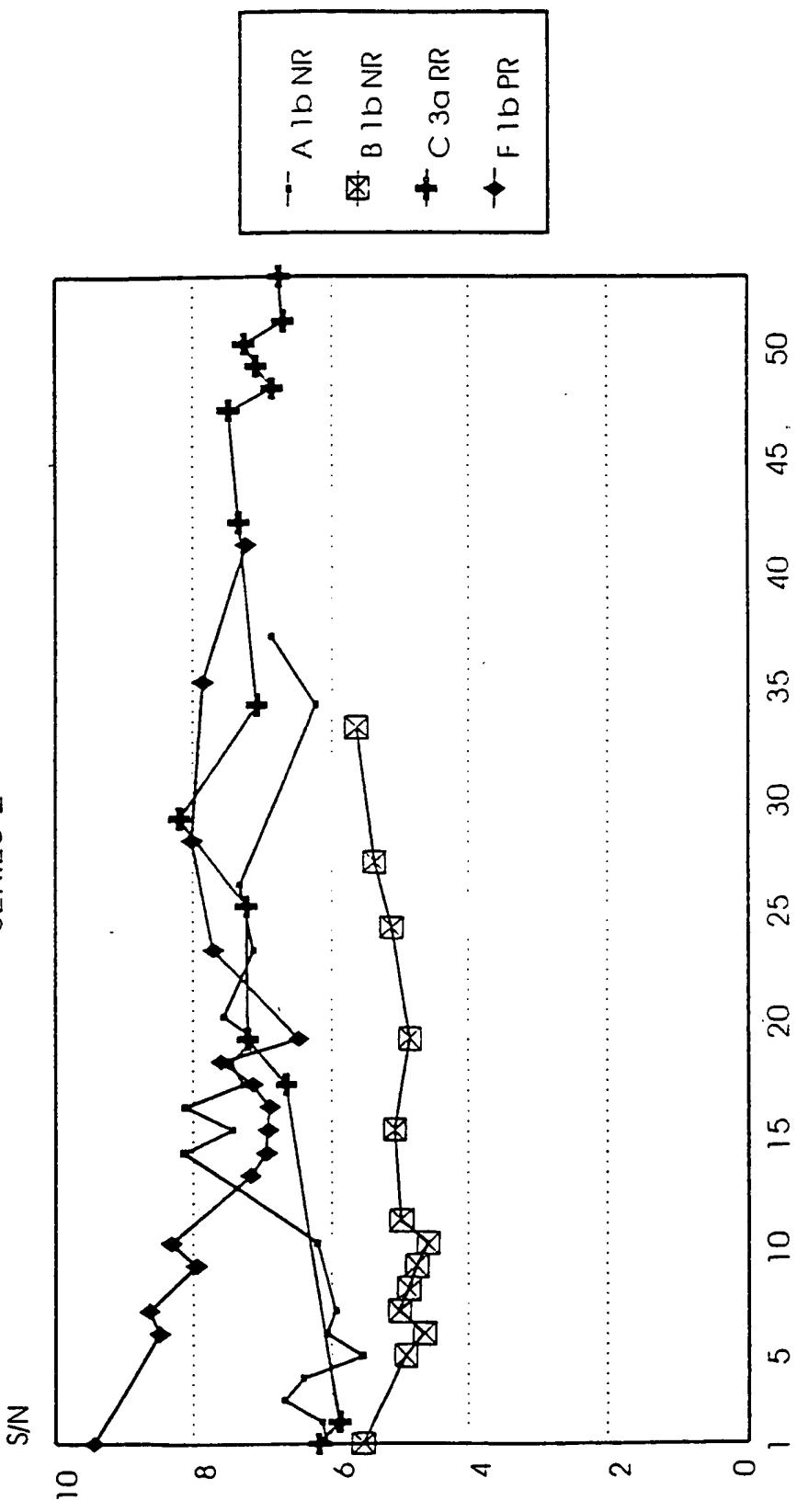


weeks after start of treatment

Fig. 10

Anti-E2 levels in INCOMPLETE responders to IFN treatment

SERIES 2



months after start of treatment

Fig. 11

Anti-E2 levels in COMPLETE responders to IFN treatment  
SERIES 2

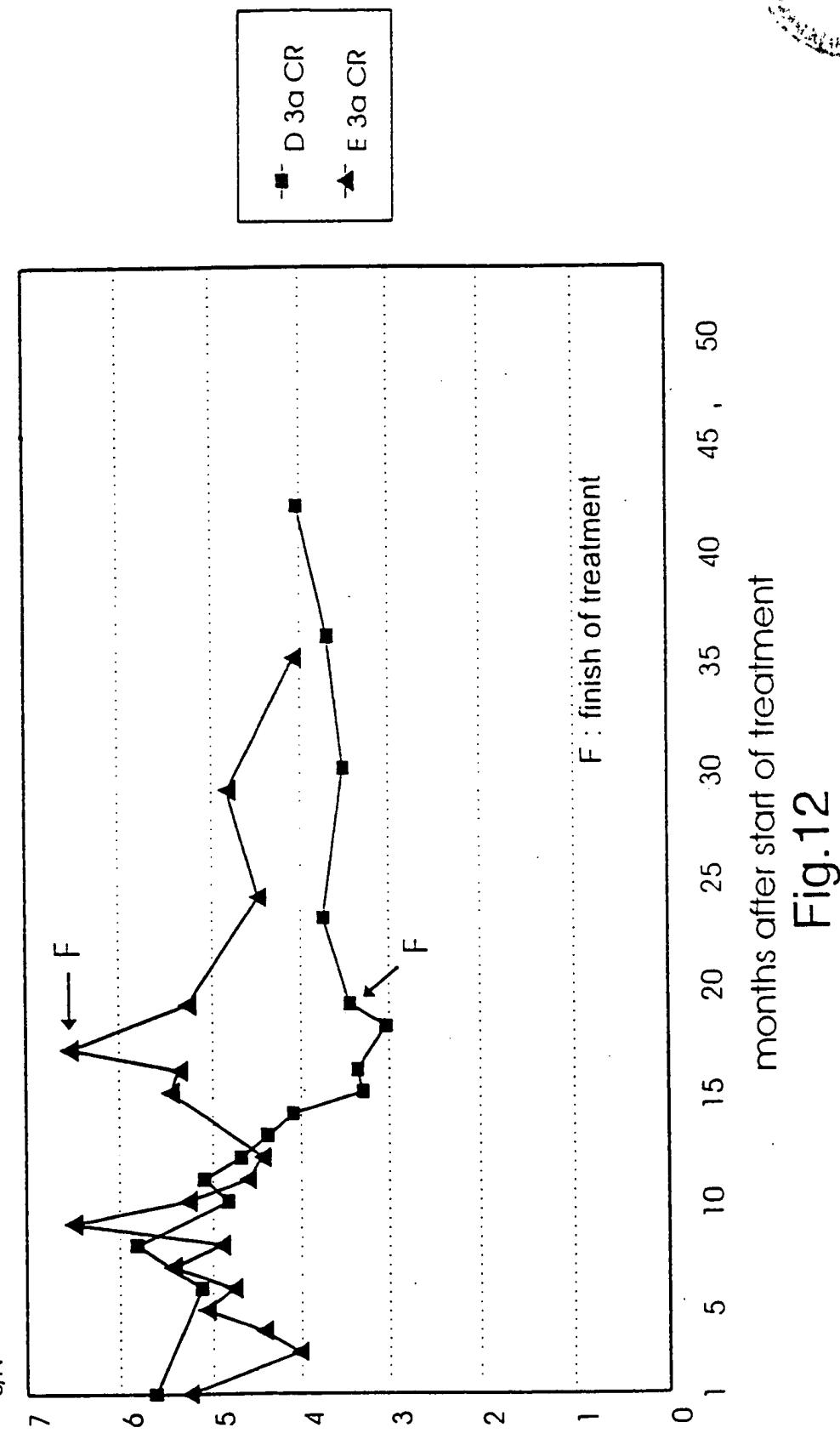


Fig.12

## Human anti-E1 reactivity competed with peptides

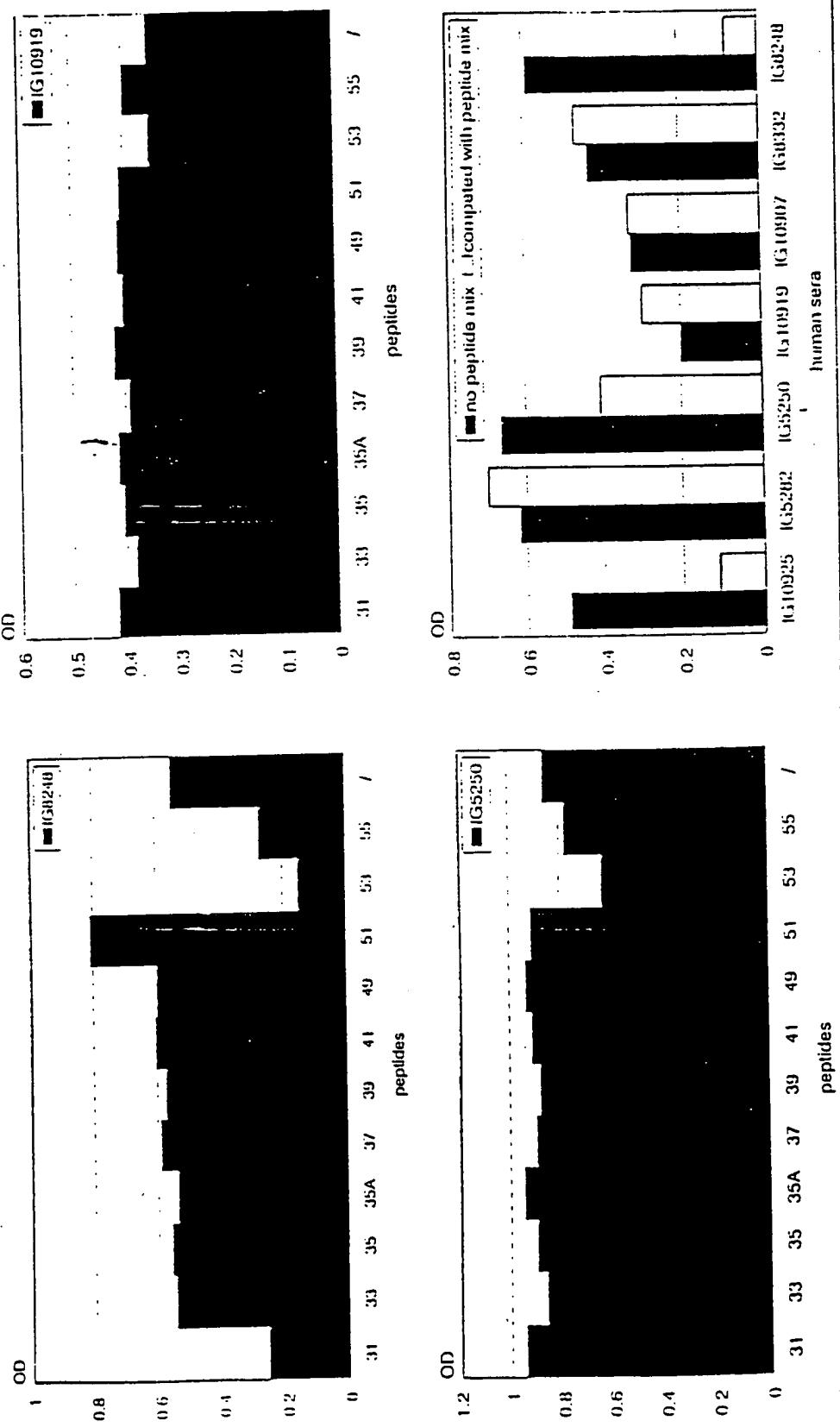


Fig.13

# Competition of reactivity of anti-E1 Mabs with peptides

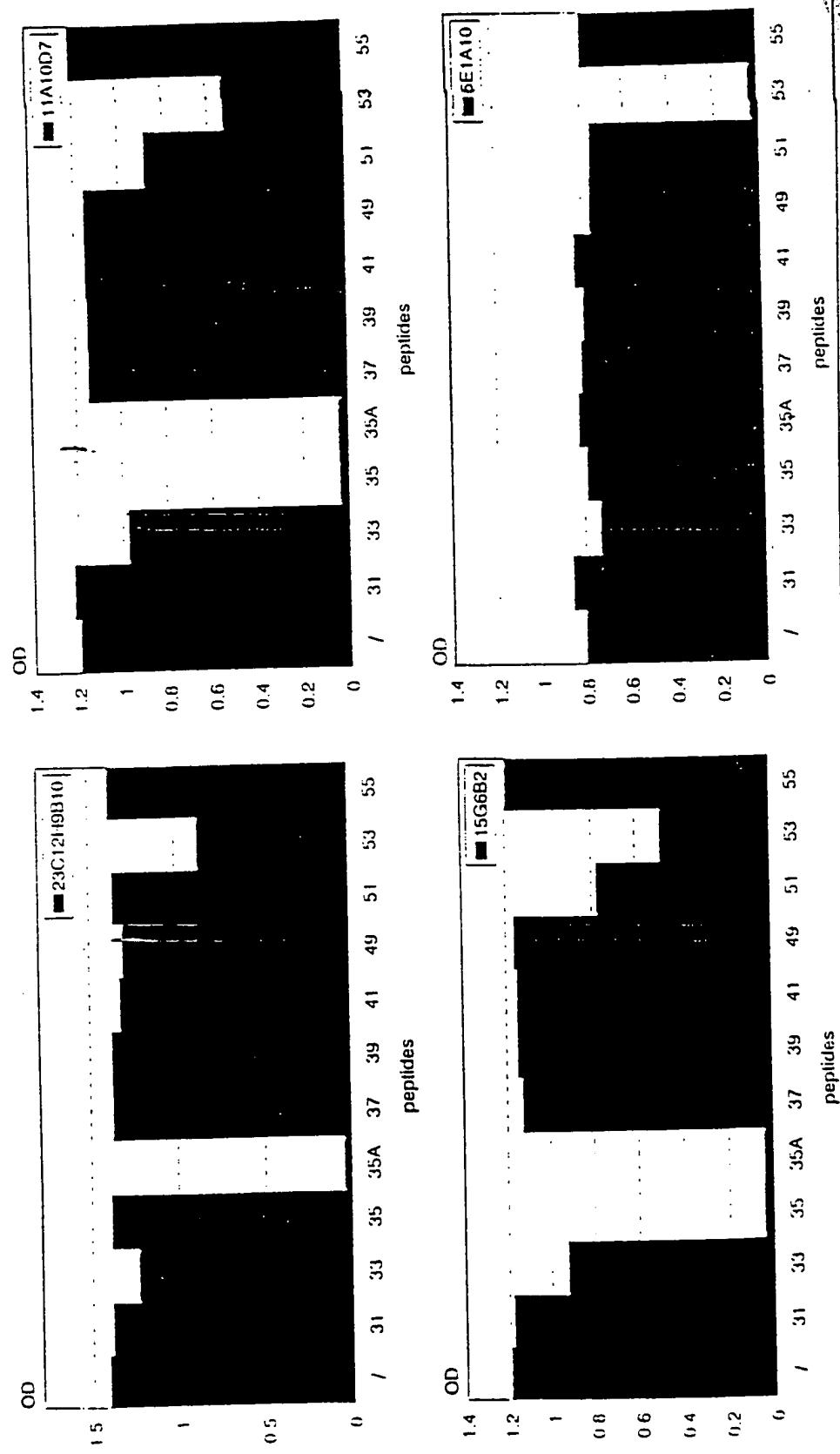


Fig.14

# Anti-E1 (epitope 1) levels in NON-RESPONDERS to IFN treatment

## SERIES 1

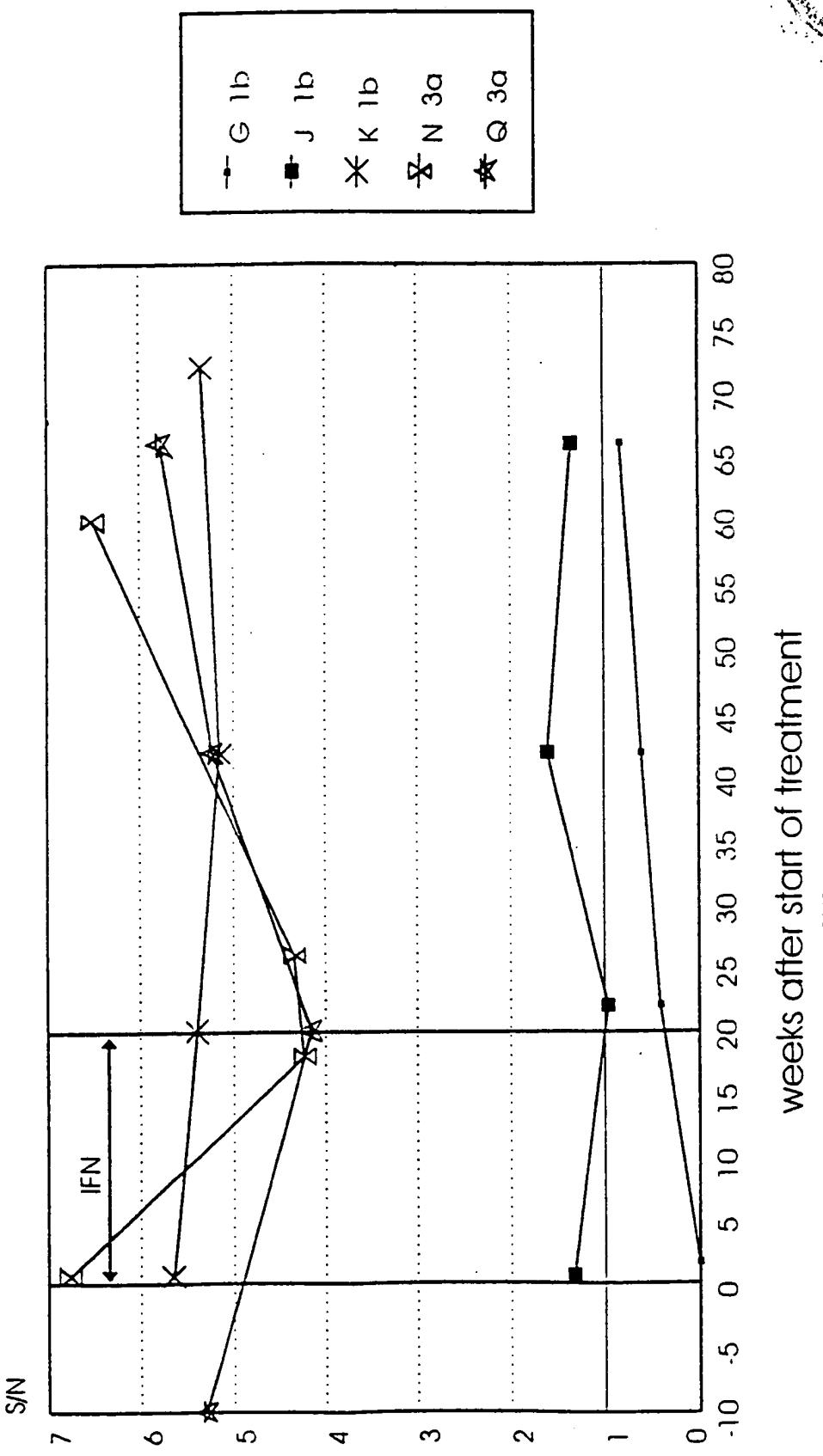


Fig. 15  
weeks after start of treatment

# Anti-E1 (epitope 1) levels in RESPONDERS to IFN treatment

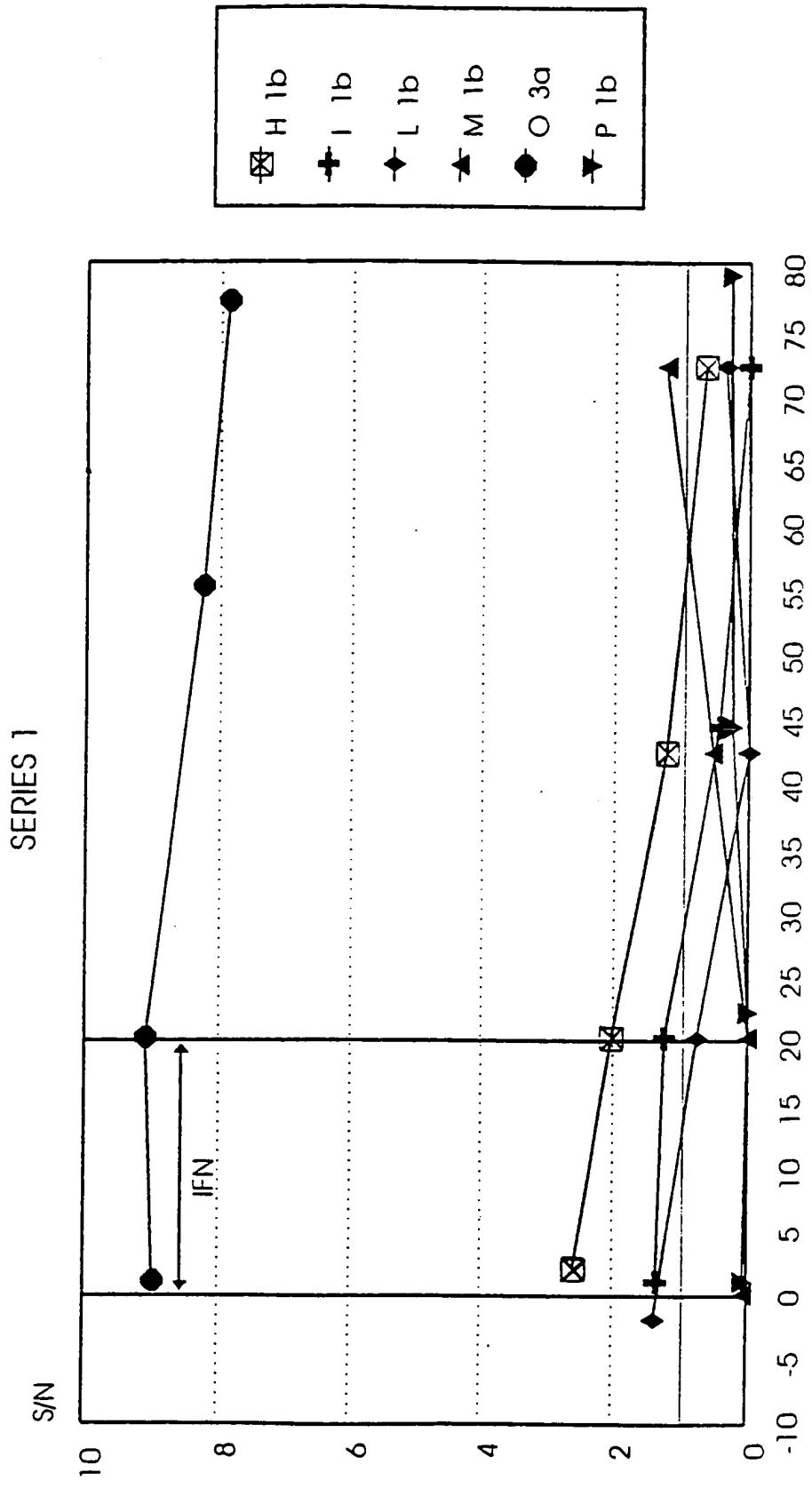
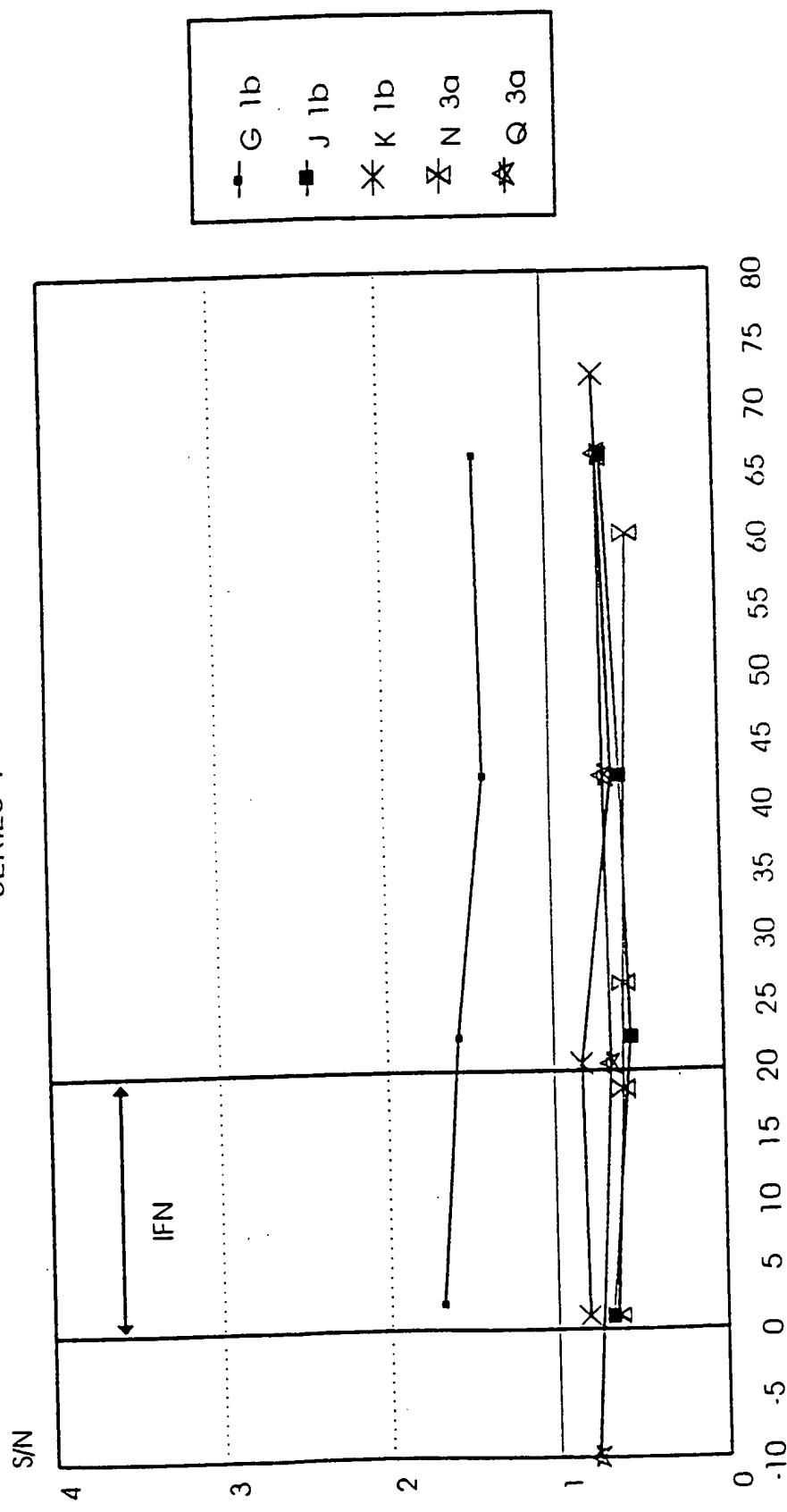


Fig. 16

Anti-E1 (epitope 2) levels in NON-RESPONDERS to IFN treatment

SERIES 1

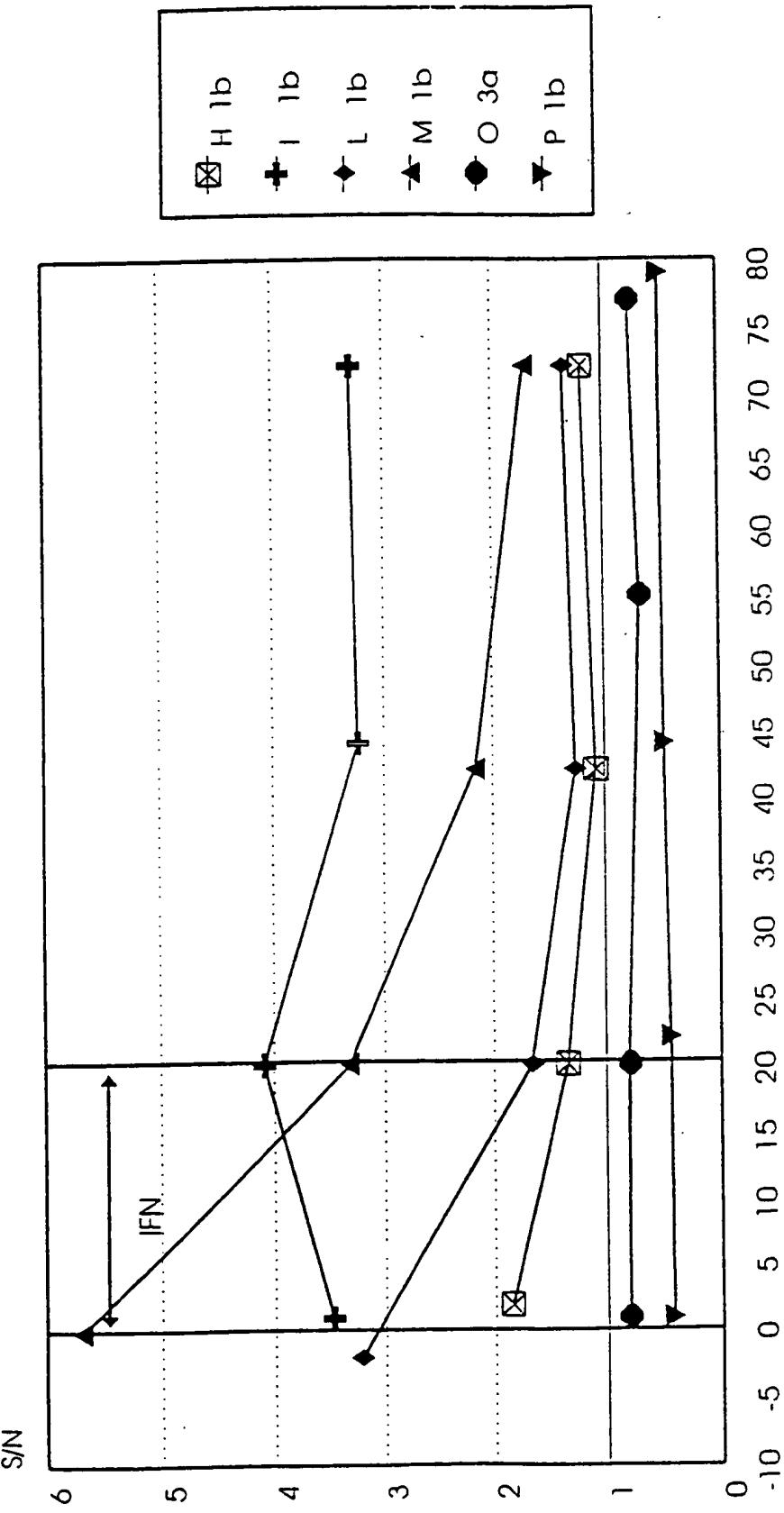


weeks after start of treatment

Fig.17

## Anti-E1 (epitope 2) levels in RESPONDERS to IFN treatment

### SERIES 1



weeks after start of treatment

Fig. 18

## Competition of reactivity of anti-E2 Mabs with peptides

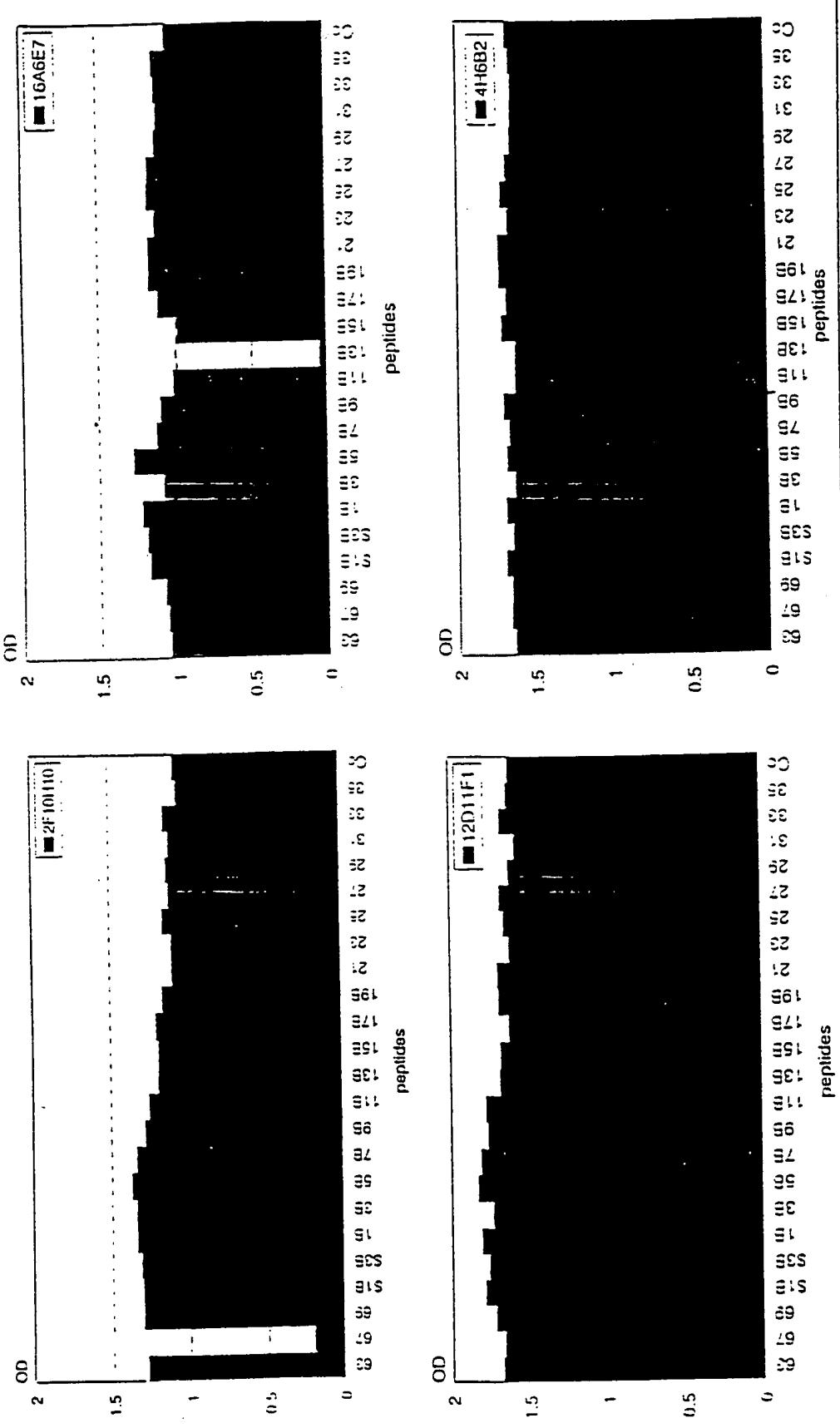


Fig.19

## Human anti-E2 reactivity competed with peptides

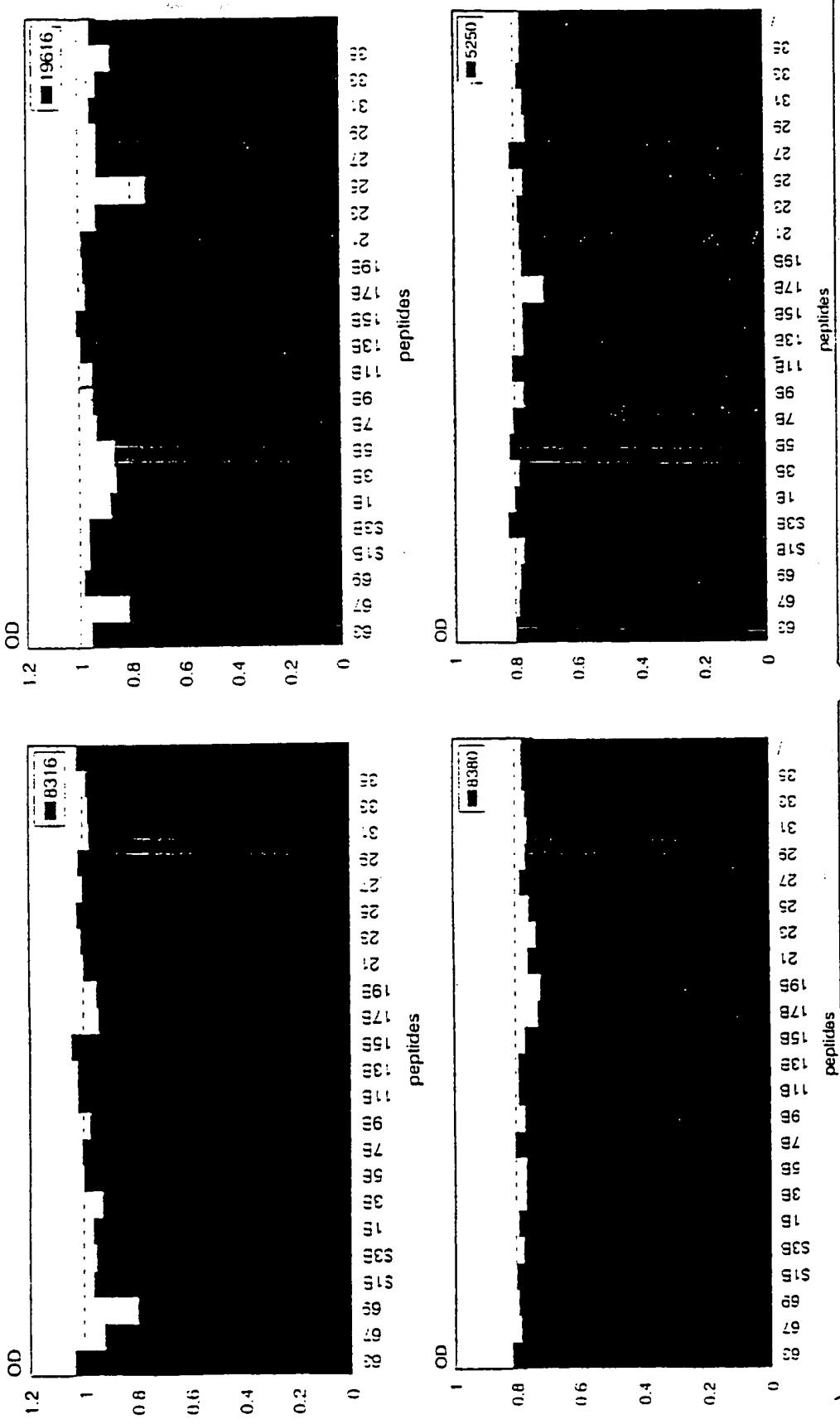


Fig. 20

# Fig. 21A

5' GGCATGCAAGCTTAATTAATT3' (SEQ ID NO 1)  
3'ACGTCCGTACGTTCGAATTAATTAATCGA5' (SEQ ID NO 94)

5'CCGGGGAGGCCTGCACGTGATCGAGGGCAGACACCATCACCAACCACATCACTAATAGT  
TAATTAACTGCA 3' (SEQ ID NO 2)  
3'CCTCCGGACGTGCACTAGCTCCGTCTGGTAGTGGTAGTGATTATCAATTAAATTG  
5' (SEQ ID NO 95)

SEQ ID NO 3 (HCCI9A)  
ATGCCCGGTTGCTCTTCTCTATCTTCCCTTGGCTTACTGTCCTGTCTGACCATTCCA  
GCTTCCGCTTATGAGGTGCGCAACGTGTCGGGATGTACCATGTCACGAACGACTGCT  
CCAACTCAAGCATTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGTGCCT  
GCCCTGCCTCGGGAGAACAAACTCTTCCCCTGCTGGTAGCGCTCACCCCCACGCTC  
GCAGCTAGGAACGCCAGCGTCCCCACCACGACAATACGACGCCACGTCGATTGCTCG  
TTGGGGCGGCTGCTCTGTTCCGCTATGTACGTGGGGATCTCTGCGGATCTGTCTTC  
CTCGTCTCCAGCTGTTACCATCTGCCCTGCCGGCATGAGACGGTGCAGGACTGCA  
ATTGCTCAATCTATCCCGGCCACATAACAGGTACCGTATGGCTGGGATATGATGAT  
GAACCTGGTCGCCCTACAACGGCCCTGGTGTATCGCAGCTGCCGGATCCCACAAGCT  
GTCGTGGACATGGTGGCGGGGCCATTGGGAGTCCTGGCGGGCTGCCCTACTATT  
CCATGGTGGGAACTGGGCTAAGGTTTGATTGTATGCTACTCTTGCTCTAATAG

SEQ ID NO 5 (HCCI10A)  
ATGTTGGTAAGGTATCGATACCCCTACATGCGGCTTCGCCGACCTCGTGGGTACA  
TTCCGCTCGTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG  
GGTTCTGGAGGACGGCGTGAACATATGCAACAGGGAAATTGCCCCTGGCTCTTCTCT  
ATCTTCCCTGGCTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGC  
CAACGTGTCGGGATGTACCATGTCACGAACGACTGCTCCAACTAAGCATTGTTAT  
GAGGCAGCGGACATGATCATGCACACCCCCGGTGCCTGCCCTGCCTGGAGAAC  
AACTCTTCCCCTGCTGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG  
TCCCCACGACAATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTCTG

# Fig. 21B

TTCCGCTATGTACGTGGGGACCTCTCGGGATCTGTCTTCCTCGTCTCCCAGCTGTTCA  
CCATCTCGCCTGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGG  
CCACATAACGGGTACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCCTACAACG  
GCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGG  
GGGCCCATTGGGGAGTCCTGGCGGGTCTGCCCTACTATTCCATGGTGGGGAACTGGGC  
TAAGGTTTGATTGTGATGCTACTCTTGCTCCCTAATAG

## SEQ ID NO 7 (HCCI11A)

ATGTTGGGAAAGGTATCGATAACCTTACGTGCGGCTTCGCCGACCTCATGGGTACA  
TTCCGCTCGCGCCCGCCCTAGGGGGTGCCTGCCAGAGCCCTGGCGCATGGCGTCCG  
GGTTCTGGAAGACGGCGTGAACATATGCAACAGGGATTGCTGGTTGCTCTTCTCTA  
TCTTCCTCTGGCTTACTGTCTGTGACCATTCCAGCTTCCGCTTATGAGGTGC  
AACGTGTCCGGATGTACCATGTCACGAACGACTGCTCCAACCTCAAGCATTGTGTATG  
AGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCTGCGTTCGGGAGAAC  
ACTCTTCCCCTGCTGGTAGCGCTACCCCCACGCTCGCAGCTAGGAACGCCAGCGT  
CCCCACTACGACAATACGACGCCACGTCGATTGCTCGTTGGGCGGCTGTTCTGTT  
CCGCTATGTACGTGGGGATCTCTGCGGATCTGCTTCCCTGCTCCAGCTGTTCA  
ATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGG  
ACATAACAGGTACCGTATGGCTTGGGATATGATGATGAACTGGTAATAG

## SEQ ID NO 9 (HCCI12A)

ATGCCCGGTTGCTCTTCTATCTTCTCTTGGCCCTGCTGTCCTGCTGACCATACCA  
GCTTCCGCTTATGAAGTGCACGCGAACGTGTCCGGGGTGTACCATGTCACGAACGACTGCT  
CCAACCTCAAGCATAGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGT  
GCCCTGCGTTGGAGGGCAACTCCTCCGTTGCTGGGTGGCGCTCACTCCCACGCTC  
GCGGCCAGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTGCTC  
GTTGGGGCTGCTGCTTCTGTTCCGCTATGTACGTGGGGATCTCTGCGGATCTGTTT  
CCTGTTCCCAGCTGTTCACCTCTCACCTGCCGGCATCAAACAGTACAGGACTGCA  
ACTGCTCAATCTATCCCGGCCATGTATCAGGTACCGCATGGCTTGGGATATGATGAT  
GAACTGGTCCTAATAG

## SEQ ID NO 11 (HCCI13A)

ATGTCCGGTTGCTCTTCTATCTTCTCTTGGCCCTGCTGTCCTGCTGACCATACCA  
GCTTCCGCTTATGAAGTGCACGCGAACGTGTCCGGGGTGTACCATGTCACGAACGACTGCT  
CCAACCTCAAGCATAGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGT

Fig. 21C

GCCTGCCTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTC  
GCGGCCAGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTC  
GTTGGGGCTGCTGCTTCTGTTCCGCTATGTACGTGGGGATCTCTGCGGATCTGTTT  
CCTTGTTCAGCTGTTCACCTCTCACCTGCCGGCATCAAACAGTACAGGACTGCA  
ACTGCTCAATCTATCCCGGCCATGTATCAGGTACCGCATGGCTGGATATGATGAT  
GAACGGTAATAG

SEQ ID NO 13 (HCCI17A)

ATGCTGGTAAAGGCCATCGATAACCCTAACGTGCGGCTTCGCCGACCTCGTGGGTACA  
TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG  
GGTCTGGAAGACGGCGTGAACTATGCAACAGGAATTGCCCTGGTGTCTTCTCTA  
TCTTCCTCTGGCTTACTGTCCTGTCAACCATTCCAGCTTCCGCTTACGAGGTGCGC  
AACGTGTCCGGATGTACCATGTCACGAACGACTGCTCAACTCAAGCATTGTGTATG  
AGGCAGCGGACATGATCATGCCACACCCCCGGTGCCTGCCCTGCCGTGGAGAAC  
ACTCTTCCCGCTGCTGGTAGCGCTACCCCCACGCTCCGGCTAGGAACGCCAGCAT  
CCCCACTACAACAATACGACGCCACGTCGATTGCTCGTTGGGGCGCTGCTTCTGTT  
CCGCTATGTACGTGGGGATCTCTGCGGATCTGTCTTCCGTCTCCAGCTGTTCA  
ATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGCC  
ACATAACGGTCACCGTATGGCTGGATATGATGATGAACTGGTACTAATAG

SEQ ID NO 15 (HCPr51)

ATGCCCGGTTGCTCTTCTATCTT

SEQ ID NO 16 (HCPr52)

ATGTTGGGTAAGGTACATCGATAACCCT

SEQ ID NO 17 (HCPr53)

CTATTAGGACCAGTTCATCATCATATCCCA

SEQ ID NO 18 (HCPr54)

CTATTACCAGTTCATCATCATATCCCA

SEQ ID NO 19 (HCPr107)

ATACGACGCCACGTCGATTCCCAGCTGTTACCCATC

# Fig. 21D

SEQ ID NO 20 (HCPr108)

GATGGTGAACAGCTGGGAATCGACGTGGCGTCGTAT

SEQ ID NO 21 (HCCI37)

ATGTTGGGTAAAGGTATCGATAACCTTACATGCGGCTTCGCCGACCTCGTGGGTACA  
TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGATGGCGTCCG  
GGTTCTGGAGGAACGGCGTGAACATATGCAACAGGAATTGCCCGTTGCTCTTCTCT  
ATCTTCCTCTTGGCTTGCTGCTGTGACCGTTCCAGCTTCCGCTTATGAAGTGC  
CAACGTGTCCGGATGTACCATGTACGAACGACTGCTCCAACTAAGCATTGTGTAT  
GAGGCAGCGGACATGATCATGCACACCCCCGGTGCCTGCCCTGCCTCGGGAGAAC  
AACTCTTCCCCTGCTGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG  
TCCCCACCACGACAATACGACGCCACGTCGATTCCCAGCTGTTCACCATCTCGCCTCG  
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCGGCCACATAACGGGT  
CACCGTATGGCTTGGATATGATGATGAACTGGTCGCCTACAAACGGCCCTGGTGGTAT  
CGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGGGGGGGGCCATTGGGG  
AGTCCTGGCGGGTCTGCCTACTATTCCATGGTGGGAACGGGCTAAGGTTTGATTG  
TGATGCTACTCTTGCTCCCTAATAG

SEQ ID NO 23 (HCCI38)

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TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGATGGCGTCCG  
GGTTCTGGAGGAACGGCGTGAACATATGCAACAGGAATTGCCCGTTGCTCTTCTCT  
ATCTTCCTCTTGGCTTGCTGCTGTGACCGTTCCAGCTTCCGCTTATGAAGTGC  
CAACGTGTCCGGATGTACCATGTACGAACGACTGCTCCAACTAAGCATTGTGTAT  
GAGGCAGCGGACATGATCATGCACACCCCCGGTGCCTGCCCTGCCTCGGGAGAAC  
AACTCTTCCCCTGCTGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG  
TCCCCACCACGACAATACGACGCCACGTCGATTCCCAGCTGTTCACCATCTCGCCTCG  
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCGGCCACATAACGGGT  
CACCGTATGGCTTGGATATGATGATGAACTGGTAA  
TAG

SEQ ID NO 25 (HCCI39)

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TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGATGGCGTCCG  
GGTTCTGGAGGAACGGCGTGAACATATGCAACAGGAATTGCCCGTTGCTCTTCTCT

# Fig. 21E

ATCTTCCTCTTGGCTTGCTGTCCTGTCAGCCGTTCCAGCTTCCGCTTATGAAGTGCG  
CAACGTGTCCGGATGTACCATGTCACGAACGACTGCTCCAACCTAAGCATTGTGTAT  
GAGGCAGCGGACATGATCATGCACACCCCCGGTGCCTGCCCTGCGTTCGGAGAAC  
AACTCTTCCCGCTGCTGGTAGCGCTACCCCCACGCTCGCAGCTAGGAACGCCAGCG  
TCCCCACCACGACAATAACGACGCCACGTCGATTCCAGCTGTTACCATCTGCCCTCG  
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT  
CACCGTATGGCTTGGATATGATGATGAACGGTGCCTACAACGGCCCTGGTGGTAT  
CGCAGCTGCTCCGGATCCTCTAATAG

SEQ ID NO 27 (HCC140)

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TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG  
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ATCTTCCTCTTGGCTTGCTGTCCTGTCAGCCGTTCCAGCTTCCGCTTATGAAGTGCG  
CAACGTGTCCGGATGTACCATGTCACGAACGACTGCTCCAACCTAAGCATTGTGTAT  
GAGGCAGCGGACATGATCATGCACACCCCCGGTGCCTGCCCTGCGTTCGGAGAAC  
AACTCTTCCCGCTGCTGGTAGCGCTACCCCCACGCTCGCAGCTAGGAACGCCAGCG  
TCCCCACCACGACAATAACGACGCCACGTCGATTCCAGCTGTTACCATCTGCCCTCG  
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT  
CACCGTATGGCTTGGATATGATGATGAACGGTGCCTACAACGGCCCTGGTGGTAT  
CGCAGCTGCTCCGGATCGTATCGAGGGCAGACACCATCACCACTAATAG

SEQ ID NO 29 (HCC162)

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CCTTGAAGACGGATAAATTGCAACAGGGATTGCCCCGGTTGCTCCTTTCTATT  
TCCTTCTCGCTCTGTTCTTGCTTAATTCCAGCAGCTAGTCTAGAGTGGCGGAAT  
ACGTCTGGCCTCTATGTCCTTACCAACGACTGTTCAATAGCAGTATTGTGTACGAGGC  
CGATGACGTTATTCTGCACACACCCGGCTGCATAACCTTGTCCAGGACGGCAATACA  
TCCACGTGCTGGACCCCCAGTGACACCTACAGTGGCAGTCAAGTACGTGCGGAGCAACCA  
CCGCTTCGATAACGCACTGTCATGTGGACCTATTAGTGGCGCCACGATGTGCTCTGC  
GCTCTACGTGGGTGACATGTGTGGGGCTGCTTCCTCGTGGGACAAGCCTCACGTTCA  
GACCTCGTCGCCATCAAACGGTCCAGACCTGTAACGTGCTGCTGTACCCAGGCCATCT  
TTCAGGACATCGAATGGCTTGGATATGATGATGAACGGTAATAG

# Fig. 21F

SEQ ID NO 31 (HCCI63)

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CCTGAGGACGGGTAAACTATGCAACAGGAATTACCCGGTTGCTCTTCTATCT  
TTATTCTTGCCTCTCGTGTCTGACCGTTCCGGCTCTGCAGTCCCTACCGAAATG  
CCTCTGGATTATCATGTTACCAATGATTGCCAAACTCTTCCATAGTCTATGAGGCA  
GATAACCTGATCCTACACGCACCTGGTTGCGTGCCTTGTGTCATGACAGGTAATGTGA  
GTAGATGCTGGTCCAAATTACCCCTACACTGTCAGCCCCGAGCCTCGGAGCAGTCAC  
GGCTCCTCTCGGAGAGCCGTTGACTACCTAGCGGGAGGGCTGCCCTCTGCTCCGCG  
TTATACGTAGGAGACCGTGTGGGCACTATTCTGGTAGGCCAAATGTTCACCTATA  
GGCCTGCCAGCACGCTACGGTGCAGAACTGCAACTGTTCCATTACAGTGGCCATGT  
TACCGGCCACCGGATGGATGGATGATGAACTGGTAATAG

SEQ ID NO 33 (HCPr109)

TGGGATATGATGATGAACTGGTC

SEQ ID NO 34 (HCPr72)

CTATTATGGTGGTAAKGCCARCARCAGAGCAGGAG

SEQ ID NO 35 (HCCL22A)

TGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTCC  
GGATCCCACAAGCTGTCGTGGACATGGTGGGGGGCCATTGGGGAGTCCTGGCGG  
GCCTCGCCTACTATTCCATGGTGGGAACTGGCTAAGGTTTGGTTGTATGCTACTC  
TTGCCGGCGTCGACGGGATACCCCGTGTCAAGGAGGGCAGCAGCCTCCGATAACCA  
GGGGCCTTGTGTCCCTCTTAGCCCCGGTCGGCTCAGAAAATCCAGCTCGTAAACAC  
CAACGGCAGTTGGCACATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAAC  
AGGGTTCTTGGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAG  
CGCTTGGCCAGCTGTCGCTCATCGACAAGTTGCTCAGGGTGGGTCCCTCACTT  
ACACTGAGCCTAACAGCTGGACCAGAGGCCACTGCTGGCACTACGGCCTCGACC  
GTGTGGTATTGTACCCCGTCTCAGGTGTGGTCCAGTGTATTGCTTCACCCGAGCC  
CTGTTGGTGGTGGGACGACCGATGGTTGGTGTCCCCACGTATAACTGGGGGGCGAA  
CGACTCGGATGTGCTGATTCTCAACAAACACGCGGCCGCGAGGCAACTGGTTCGGC  
TGTACATGGATGAATGGCACTGGTTACCAAGACGTGTGGGGCCCCCGTGAACA  
TCGGGGGGGGCGGCAACAAACACCTTGACCTGCCCACTGACTGTTTCGGAAGCACCC  
CGAGGCCACCTACGCCAGATGCGTTCTGGCCCTGGCTGACACCTAGGTGTATGGTT

Fig. 21G

CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAGGT  
TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTGAAGCCGATGCAATTGGACTCG  
AGGAGAGCGTTGTGACTGGAGGACAGGGATAGATCAGAGCTTAGCCCCGCTGCTGCTG  
TCTACAACAGAGTGGCAGATACTGCCCTGTTCTTCAACCACCCCTGCCGGCCCTATCCA  
CCGGCCTGATCCACCTCCATCAGAACATCGTGGACGTGCAATACCTGTACGGTAGG  
GTCGGCGGTTGTCTCCCTGTCAATGGAGTATGTCCTGTTGCTCTCCTCTCCT  
GGCAGACCGCGCGCATCTGCCCTGCTTATGGATGATGCTGCTGATAGCTAAGCTGAG  
GCCGCCCTAGAGAACCTGGTGGTCCTCAATGCCGGCCGTTGGCCGGCGCATGGC  
ACTCTTCCCTCCTGTGTTCTGTGCTGCCCTGGTACATCAAGGGCAGGCTGGTCCC  
TGGTGCAGGACATACGCCCTCATGGCGTGTGGCCGCTGCTCCTGCTTCTGCTGGCCTTAC  
CACCAACGAGCTTATGCCCTAGTAA

SEQ ID NO 37 (HCCI41)

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TTGCCGGCGTCGACGGGCAACCCGGTGTCAAGGAGGGCAGCAGCCTCCGATAACCA  
GGGGCCTTGTGTCCTCTTTAGCCCCGGTCGGCTCAGAAAATCCAGCTCGTAAACAC  
CAACGGCAGTTGGCACATCAACAGGACTGCCCTGAACGTGCAACGACTCCCTCCAAAC  
AGGTTCTTGCCGCACATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAG  
CGCTTGGCCAGCTGTCGCTCATCGACAAGTCGCTCAGGGTGGGGTCCCCTCACTT  
ACACTGAGCCTAACAGCTGGACCAAGAGGCCACTGCTGGACTACGCCCTCGACC  
GTGTGGTATTGTACCCCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCC  
CTGTTGTGGTGGGACGACCGATCGGTTGGTGTCCCCACGTATAACTGGGGGGCGAA  
CGACTCGGATGTGCTGATTCTCAACAAACACGCCGCCGCCGAGGCAACTGGTTGGC  
TGTACATGGATGAATGGCACTGGTTACCAAGACGTGTTGGGGCCCCCGTGCACACA  
TCGGGGGGGCCGGCAACAAACACCTTGACCTGCCCACTGACTGTTTGGAAAGCACCC  
CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTT  
CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAGGT  
TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTGAAGCCGATGCAATTGGACTCG  
AGGAGAGCGTTGTGACTGGAGGACAGGGATAGATCAGAGCTAGCCCCGCTGCTGCTG  
TCTACAACAGAGTGGCAGAGTGGCAGAGCTTAATTAAATTAG

SEQ ID NO 39 (HCCI42)

GATCCCACAAGCTGTCGTGGACATGGTGGCGGGGCCATTGGGGAGTCCTGGCGGG  
CCTCGCCTACTATTCCATGGTGGGAACCTGGCTAAGGTTTGGTTGTATGCTACTCT

# Fig. 21H

TTGCCGGCGTCGACGGGCATACCGCGTGTCAAGGAGGGCAGCAGCCTCCGATACCA  
GGGCCTTGTGTCCCTCTTAGCCCCGGGCGCTCAGAAAATCCAGCTCGTAAACAC  
CAACGGCAGTTGGCACATCAACAGGACTGCCCTGAAC TGCAACGACTCCCTCCAAAC  
AGGGTTCTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAG  
CGCTTGGCCAGCTGTCGCTCCATCGACAAGTTGCTCAGGGTGGGTCCCCTCACTT  
ACACTGAGCCTAACAGCTCGGACCAGAGGCCACTGCTGGCACTACGCGCCTCGACC  
GTGTGGTATTGTACCCCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCC  
CTGTTGTGGTGGGACGACCGATCGGTTGGTGTCCCCACGTATAACTGGGGGGCGAA  
CGACTCGGATGTGCTGATTCTAACAAACACGCGGCCGCGAGGCAACTGGTTCGGC  
TGTACATGGATGAATGGCACTGGGTTACCAAGACGTGTGGGGGGGGGGCGTGCACAA  
TCGGGGGGGGCGGCAACAAACACCTTGACCTGCCCACTGACTGTTTCGGAAGCACCC  
CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTT  
CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTACCCATCTCAAGGT  
TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTGAAAGCCGATGCAATTGGACTCG  
AGGAGAGCGTTGTGACTGGAGGACAGGGATAGATCAGAGCTTAGCCCCTGCTGCTG  
TCTACAAACAGGTGATCGAGGGCAGACACCACCACTACCAACTAAAG

SEQ ID NO 41 (HCC143)

ATGGTGGGAACTGGCTAACGGTTGGTGTGATGCTACTCTTGCCGGCGTCGACG  
GGCATACCCCGTGTCAAGGAGGGCAGCAGCCTCCGATACCAAGGGCCTTGTGTCCT  
CTTAGCCCCGGTGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC  
ATCAACAGGACTGCCCTGAAC TGCAACGACTCCCTCCAAACAGGGTTCTTGCCGAC  
TATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAGCGCTTGGCCAGCTGTCG  
CTCCATCGACAAGTTGCTCAGGGTGGGTCCCTCACTTACACTGAGCCTAACAGC  
TCGGACCAGAGGCCACTGCTGGCACTACGCGCCCTGACCGTGTGGTATTGTACCCG  
CGTCTCAGGTGTGCGGTCCAGTGTATTGCTTACCCCGAGCCCTGTTGTGGTGGGAC  
GACCGATGGTTGGTGTCCCCACGTATAACTGGGGGGCAACGACTCGGATGTGCTG  
ATTCTCAACAAACACGCGGCCGCCGAGGCAACTGGTTGGCTGTACATGGATGAATG  
GCACTGGTTACCAAGACGTGTGGGGCCCCCGTGCACACATCGGGGGGGCGGCA  
ACAACACCTTGACCTGCCCACTGACTGTTTGGGAAGCACCCGAGGCCACCTACGC  
CAGATGCGGTTCTGGCCCTGGCTGACACCTAGGTGTATGGTTATTACCCATATAGG  
CTCTGGCACTACCCCTGCACTGTCAACTCACCACATTCAAGGTTAGGATGTACGTGG  
GGCGTGGAGCACAGGTTGCAAGCCGATGCAATTGGACTCGAGGAGAGCGTTGTGA  
CTTGGAGGACAGGGATAGATCAGAGCTTAGCCCCTGCTGCTGCTACAAACAGAGTGG  
CAGAGCTTAATTAAATTAG

# Fig. 21I

SEQ ID NO 43 (HCCI44)

ATGGTGGGAACTGGGCTAAGGTTTGGTTGTATGCTACTCTTGCCGGCGTCGACG  
GGCATACCCCGCGTGTCAAGGAGGGCAGCAGCCTCCGATACCAGGGCCTGTGTCCT  
CTTAGCCCCGGGTGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC  
ATCAACACAGGACTGCCCTGAAC TGCAACGACTCCCTCCAAACAGGGTTCTTGCCGCAC  
TATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAGCGCTTGGCCAGCTGTCG  
CTCCATCGACAAGTTGCTCAGGGTGGGTCCCTCACTTACACTGAGCCTAACAGC  
TCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC GTGTGGTATTGTACCCG  
CGTCTCAGGTGTGGTCCAGTGTTGCTTACCCGAGCCCTGTTGTGGTGGGAC  
GACCGATCGGTTGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTG  
ATTCTCAACAAACACGCGGCCGCCGAGGGCAACTGGTTCGGCTGTACATGGATGAATG  
GCACTGGTTCACCAAGACGTGTGGGGCCCCCGTGCAACATGGGGGGCCGGCA  
ACAACACCTTGACCTGCCCCACTGACTGTTTGGAAAGCACCCGAGGCCACCTACGC  
CAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTGGTCATTACCCATATAAGG  
CTCTGGCACTACCCCTGCACTGTCAACTTACCATCTCAAGGTTAGGATGTACGTGGG  
GGCGTGGAGCACAGGTTGCAAGCCGATGCAATTGGACTCGAGGAGAGCGTTGTGA  
CTTGGAGGACAGGGATAGATCAGAGCTTAGCCGCTGCTGTACAAACAGGTGAT  
CGAGGGCAGACACCATCACCAACCATCACTAATAG

SEQ ID NO 45 (HCCL64)

ATGGTGGCGGGGGCCATTGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGG  
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AGGACTGCCCTGAACGACTCCCTCCAAACAGGGTTCTTGCCGACTATTCT  
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GCGGTTCTGGCCCTGGCTGACACCTAGGTGTGGTCATTACCCATATAAGGCTCTGG  
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Fig. 21J

TGGAGCACAGGTTCGAAGCCGATGCAATTGGACTCGAGGAGAGCGTTGTACTTGGAG  
GGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTACAACACAGAGTGGCAGATA  
CTGCCCTGTTCTTCACCACCCCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCA  
GAACATCGTGGACGTGCAATACCTGTACGGTAGGGTCGGCGGTTGTCCTCCCTGTC  
ATCAAATGGGAGTATGTCCTGTTGCTCTTCTCTGGCAGACGCGCGCATCTGCGC  
CTGCTTATGGATGATGCTGCTGATAAGCTGAGGCGCCTAGAGAACCTGGTG  
GTCCTCAATGCGGCGGCCGTGGCCGGGCGCATGGCACTCTTCCTCCTGTGTTCTT  
CTGTGCTGCCTGGTACATCAAGGGCAGGCTGGTCCCTGGTGGCATAACGCCTCTAT  
GGCGTGTGGCGCTGCTCCTGCTGGCCTTACCACCACGAGCTTATGCCTAGTAA

SEQ ID NO 47 (HCC165)

AATTTGGTAAGGTATCGATACCCCTACATGCGGCTTCGCCGACCTCGTGGGTACA  
TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG  
GGTTCTGGAGGACGGCGTGAACATATGCAACAGGGAAATTGCCCGGTTGCTCTTCTCT  
ATCTTCCTCTGGCTTGCTGCTGTCTGACCGTTCCAGCTCCGTTATGAAGTGCG  
CAACGTGTCCGGATGTACCATGTACGAACGACTGCTCCAACCTCAÁGCATTGTGTAT  
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCTGCGTTGGGAGAAC  
AACTCTTCCCCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG  
TCCCCACCACGACAATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTCTG  
TTCCGCTATGTACGTGGGGACCTCTCGGATCTGTCTTCCTCGTCTCCAGCTGTTCA  
CCATCTCGCCTGCCGGCATGAGACGGTGAGGACTGCAATTGCTCAATCTATCCGG  
CCACATAACGGGTACCGTATGGCTGGATATGATGATGAACCTGGTGCCTACAACG  
GCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGCGTGGACATGGTGGCG  
GGGCCATTGGGAGTCCTGGCGGGCTCGCCTACTATTCCATGGTGGGGACTGGG  
TAAGGTTTGGTTGTGATGCTACTCTTGCCGGCGTCACGGGATACCCGCGTGTCA  
GAGGGGAGCAGCCTCCGATACCAGGGGCTTGTGTCCTCTTAGCCCCGGGCG  
TCAGAAAATCCAGCTGTAACACCAACGGCAGTTGGCACATCAACAGGACTGCCCT  
GAAC TGCAACGACTCCCTCCAAACAGGGTTCTTGCCGCACTATTCTACAAACACAAA  
TTCAACTCGTCTGGATGCCAGAGCGCTTGGCCAGCTGTCGCTCCATGACAAGTTCG  
CTCAGGGGTGGGTCCCTCACTTACACTGAGCCTAACAGCTGGACCAGAGGCCCTA  
CTGCTGGACTACGCCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGT  
CCAGTGTATTGCTTCACCCGAGCCCTGTTGTGGTGGGACGACCGATCGTTGGTGT  
CCCCACGTATAACTGGGGGGCAACGACTCGGATGTGCTGATTCTCAACAAACACGCGG  
CCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGGTTCACCAAGA  
CGTGTGGGGCCCCCGTGCACATCGGGGGCGGCAACAAACACCTTGACCTGCC

Fig. 21K

CCACTGACTGTTTGGAAAGCACCCGAGGCCACCTACGCCAGATCGGTTCTGGCC  
CTGGCTGACACCTAGGTGTATGGTCATTACCCATATAGGCTCTGGCACTACCCCTGCA  
CTGTCAACTTCACCATCTCAAGGTTAGGATGTACGTGGGGGGCGTGGAGCACAGGTT  
CGAAGCCGCATGCAATTGGACTCGAGGGAGAGCGTTGTGACTTGAGGACAGGGATAG  
ATCAGAGCTTAGCCCGCTGCTGCTACAACAGAGTGGCAGATACTGCCCTGTTCC  
TTCACCACCCCTGCCGGCCCTATCCACCGGCTGATCCACCTCCATCAGAACATCGTGG  
ACGTGCAATACCTGTACGGTGTAGGGTCGGCGGTTGTCTCCCTGTATCAAATGGGA  
GTATGTCCTGTTGCTCTTCCTCTGGCAGACGCGCGATCTGCGCCTGCTTATGGA  
TGATGCTGCTGATAGCTCAAGCTGAGGCCGCCCTAGAGAACCTGGTGGTCCCTCAATGC  
GGCGGCCGTGGCCGGGGCGCATGGCACTCTTCCTCCTGTGTTCTCTGTGCTGCCT  
GGTACATCAAGGGCAGGCTGGTCCCTGGTGGCGCATACGCCCTATGGCGTGTGGCC  
GCTGCTCCTGCTTCTGCTGGCCTTACCAACCACGAGCTTATGCCTAGTAAGCTT

SEQ ID NO 49 (HCCI66)

ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCCAACCGCCGCCA  
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GCAGGGGCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAAC  
CTCGTGGAGGCAGAACCTATCCCCAAGGCTGCCGACCCGAGGGTAGGGCCTGGG  
CTCAGCCCAGGTTACCCCTGGCCCTCTATGGCAATGAGGGATGGGTGGCAGGATG  
GCTCTGTACCCCGCGGCTCTCGGCTAGTTGGGCCCTACAGACCCCGCGTAGG  
TCGCGTAATTGGTAAGGTATCGATACCCCTACATGCGGCTTCGCCGACCTCGTGG  
GGTACATTCCGCTCGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGG  
CGTCCGGTTCTGGAGGACGGCGTGAACATGCAACAGGAAATTGCCCGTTGCTCT  
TTCTCTATCTTCCTTTGGCTTGCTGCTGTGACCGTTCCAGCTCCGTTATGAA  
GTGCGCAACGTGTCCGGATGTACCATGTCACGAACGACTGCTCCAACTAAGCATTG  
TGTATGAGGCAGCGGACATGATCATGACACACCCCGGGTGCCTGCCCTGCGTTGGGA  
GAACAACTCTCCGCTGCTGGTAGCGCTACCCCCACGCTCGCAGCTAGGAACGCC  
AGCGTCCCCACCAACGACAATACGACGCCACGTCGATTGCTCGTGGCGGCTGCTT  
TCTGTTCCGCTATGTACGTGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCAGCTG  
TTCACCATCTGCCCTGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTAC  
CCGCCACATAACGGTCACCGTATGGCTGGATATGATGATGAACTGGTGCCTAC  
AACGGCCCTGGTGGTACGCAAGCTGCTCCGGATCCCACAAGCTGCGTGGACATGGTG  
GCGGGGGCCCATTGGGAGTCCTGGCGGCCCTGCCACTATTCCATGGTGGGAACT  
GGGCTAAGGTTTGGTTGTGATGCTACTCTTGCCGGCGTCACGGGCATACCCCGT  
GTCAGGAGGGCAGCAGCCTCCGATACCAAGGGCCTGTGCTCCCTTTAGCCCCGGG

Fig. 21L

TCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAACAGGACT  
GCCCTGAACGTCAACGACTCCCTCCAAACAGGGTTCTTGCCGACTATTCTACAAAC  
ACAAATTCAACTCGTCTGGATGCCAGAGCGCTGGCCAGCTGTCGCTCCATGACAA  
GTTCGCTCAGGGTGGGTCCCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGG  
CCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGT  
GCGGTCCAGTGTATTGCTTACCCCCGAGCCCTGTTGTGGTGGGACGACCGATCGGTT  
TGGTGTCCCCACGTATAACTGGGGGGGAACGACTCGGATGTGCTGATTCTAACAAAC  
ACGCGGCCGCGCGAGGCAACTGGTCGGCTGTACATGGATGAATGGCACTGGTTCA  
CCAAGACGTGTGGGGCCCCCGTGCAACATCGGGGGGGCGGAAACAACACCTTGA  
CCTGCCCCACTGACTGTTTGGAAAGCACCCCGAGGCCACCTACGCCAGATCGGTT  
TGGGCCCTGGCTGACACCTAGGTGTATGGTCATTACCCATATAGGCTCTGGCACTAC  
CCCTGCACTGTCAACTTACCATCTTCAAGGTTAGGATGTACGTGGGGCGTGGAGC  
ACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGGAGAGCGTTGTGACTTGGAGGACA  
GGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATACTGCC  
CTGTTCTTCACCACCCCTGCCGCCCTATCCACCGGCCTGATCCACCTCCATCAGAAC  
ATCGTGGACGTGCAATACTGTACGGTAGGGTCGGCGGTTGTCTCCCTGTATCA  
AATGGGAGTATGTCCTGTTGCTCTCCTCTGGCAGACGCGCGCATCTGCCCTGC  
TTATGGATGATGCTGCTGATAGCTCAAGCTGAGGCCGCCCTAGAGAACCTGGTGGTCC  
TCAATGCCGCCGCCGTGGCCGGGCCATGGCACTCTTCCTCCTGTGTTCTCTGT  
GCTGCCCTGGTACATCAAGGGCAGGCTGGTCCCTGGTGCAGGCAACGCCCTCATGGCG  
TGTGGCCGCTGCTCCTGCTTGCTGGCCTTACCAACCACGAGCTTATGCCTAGTAA

Fig. 22

OD measured at 450 nm  
construct

Fraction	volume	dilution	39 Type 1b	40 Type 1b	62 Type 3a	63 Type 5a
START	23 ml	1/20	2.517	1.954	1.426	1.142
FLOW THROUGH	23 ml	1/20	0.087	0.085	0.176	0.120
1	0.4 ml	1/200	0.102	0.051	0.048	0.050
2			0.396	0.550	0.090	0.067
3			2.627	2.603	2.481	2.372
4			3	2.967	3	2.694
5			3	2.810	2.640	2.154
6			2.694	2.499	1.359	1.561
7			2.408	2.481	0.347	1.390
8			2.176	1.970	1.624	0.865
9			1.461	1.422	0.887	0.604
10			1.236	0.926	0.543	0.519
11			0.981	0.781	0.294	0.294
12			0.812	0.650	0.249	0.199
13			0.373	0.432	0.239	0.209
14			0.653	0.371	0.145	0.184
15			0.441	0.348	0.151	0.151
16			0.321	0.374	0.098	0.106
17			0.525	0.186	0.099	0.108
18			0.351	0.171	0.083	0.090
19			0.192	0.164	0.084	0.087

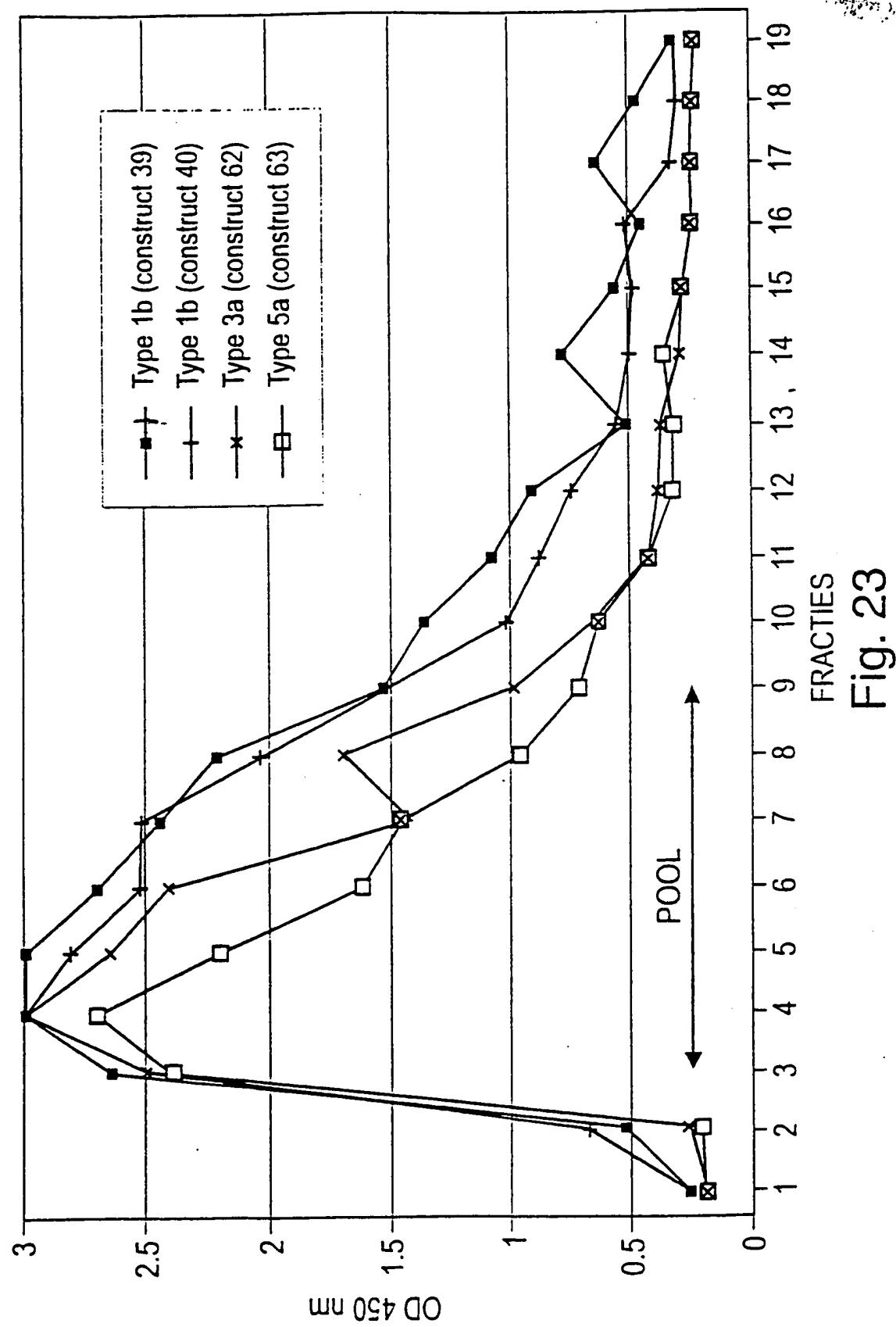


Fig. 23

Figure 24

Fraction	volume	dilution	OD measured at 450 nm			
			construct			
			39 Type 1b	40 Type 1b	62 Type 3a	63 Type 5a
20	250 $\mu$ l	1/200	0.072	0.130	0.096	0.051
21			0.109	0.293	0.084	0.052
22			0.279	0.249	0.172	0.052
23			0.093	0.151	0.297	0.054
24			0.080	0.266	0.438	0.056
25			0.251	0.100	0.457	0.048
26			3	1.649	0.722	0.066
27			3	3	2.526	0.889
28			3	3	3	2.345
29			3	3	2.849	2.580
30			2.227	1.921	1.424	1.333
31			0.263	0.415	0.356	0.162
32			0.071	0.172	0.154	0.064
33			0.103	0.054	0.096	0.057
34			0.045	0.045	0.044	0.051
35			0.043	0.047	0.045	0.046
36			0.045	0.045	0.049	0.040
37			0.045	0.047	0.046	0.048
38			0.046	0.048	0.047	0.057
39			0.045	0.048	0.050	0.057
40			0.046	0.049	0.048	0.049

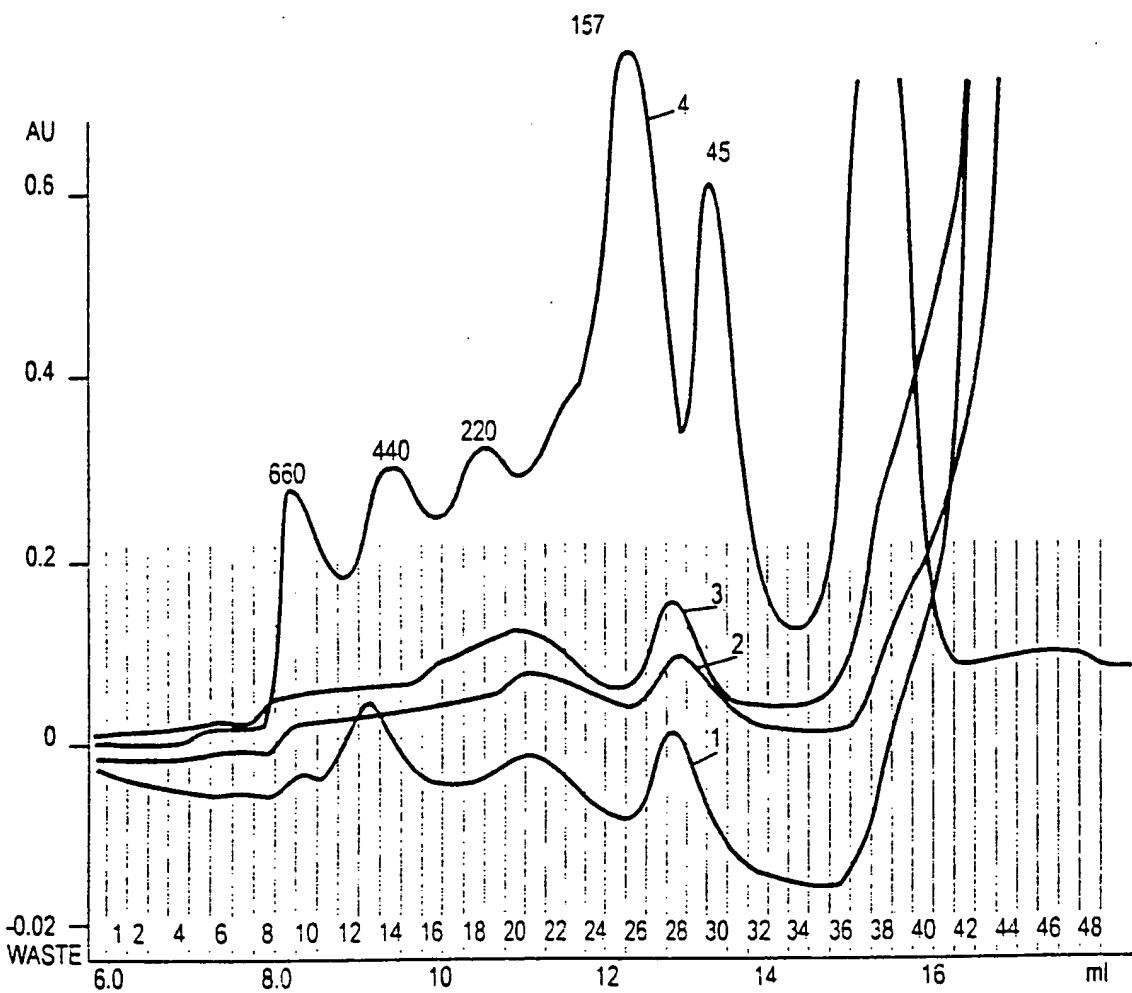


Fig. 25

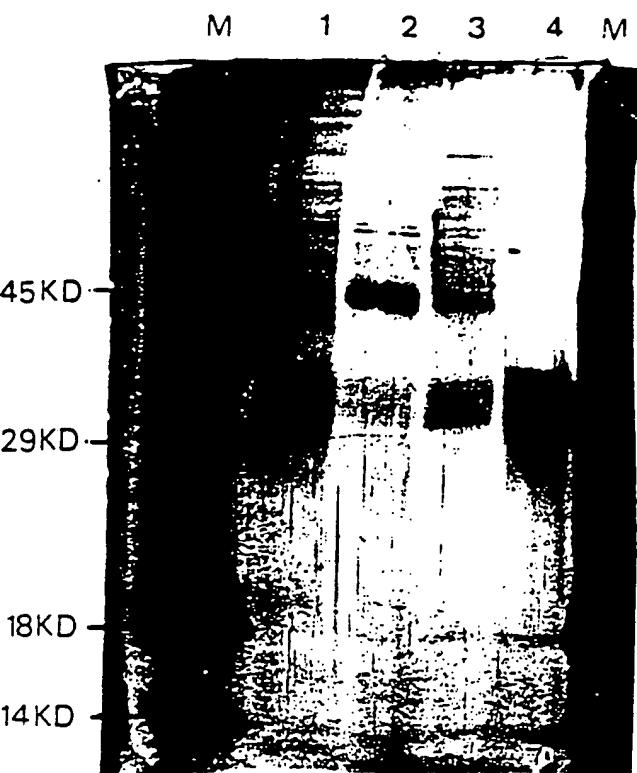


Fig. 26

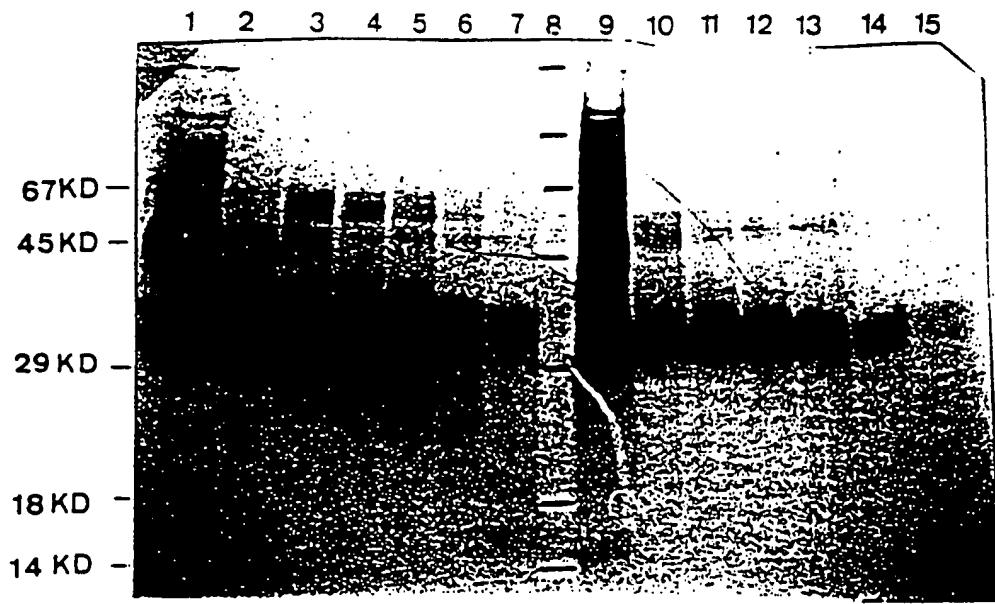


Fig. 27

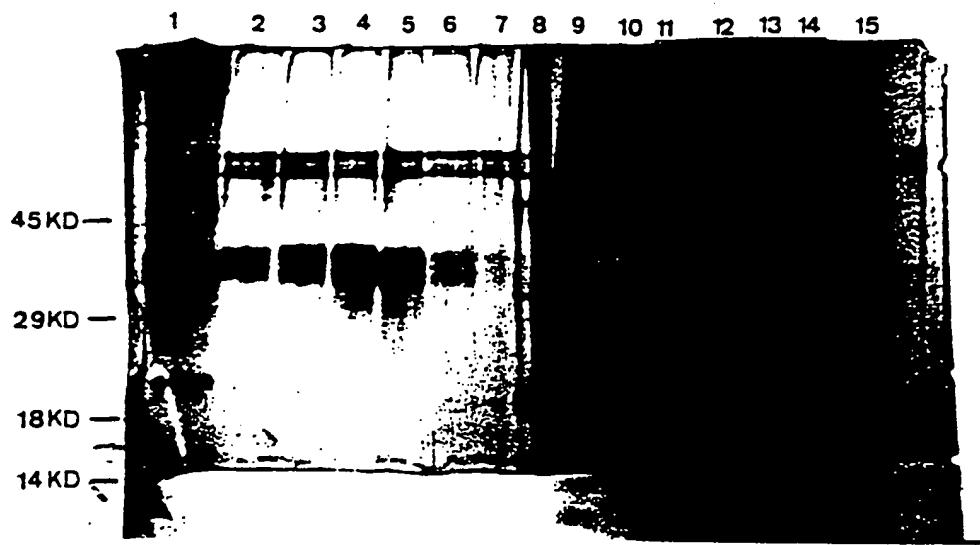


Fig.28

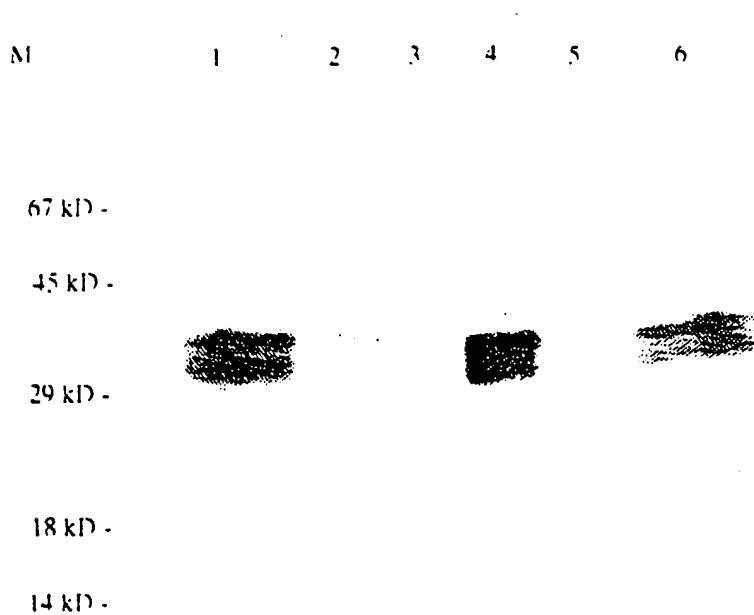


Fig.29

- Lane 1: Crude Lysate
- Lane 2: Flow through Lentil Chromatography
- Lane 3: Wash with EMPIGEN Lentil Chromatography
- Lane 4: Eluate Lentil Chromatography
- Lane 5: Flow through during concentration lentil eluate
- Lane 6: Pool of Elaster Size Exclusion Chromatography

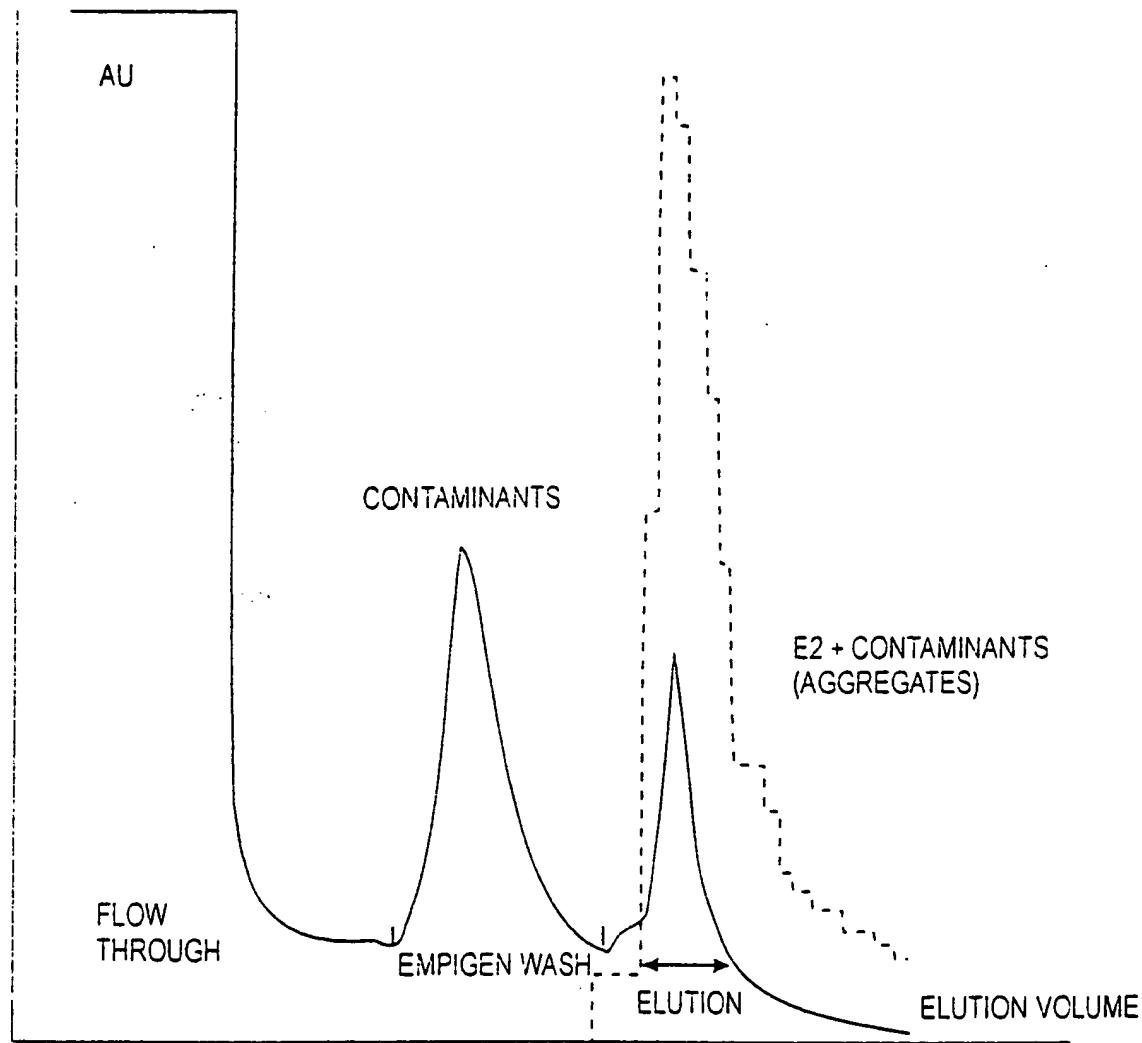
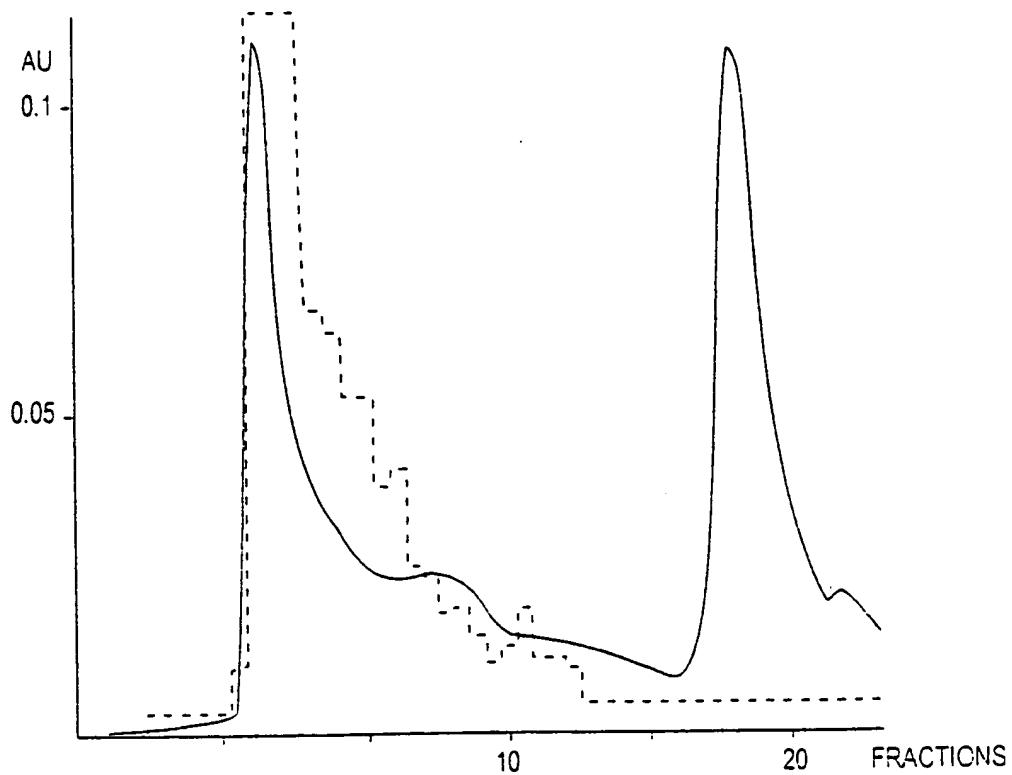


Fig. 30

NON - REDUCED

Fig. 31A

E2 + CONTAMINANTS (AGGREGATES)



REDUCED

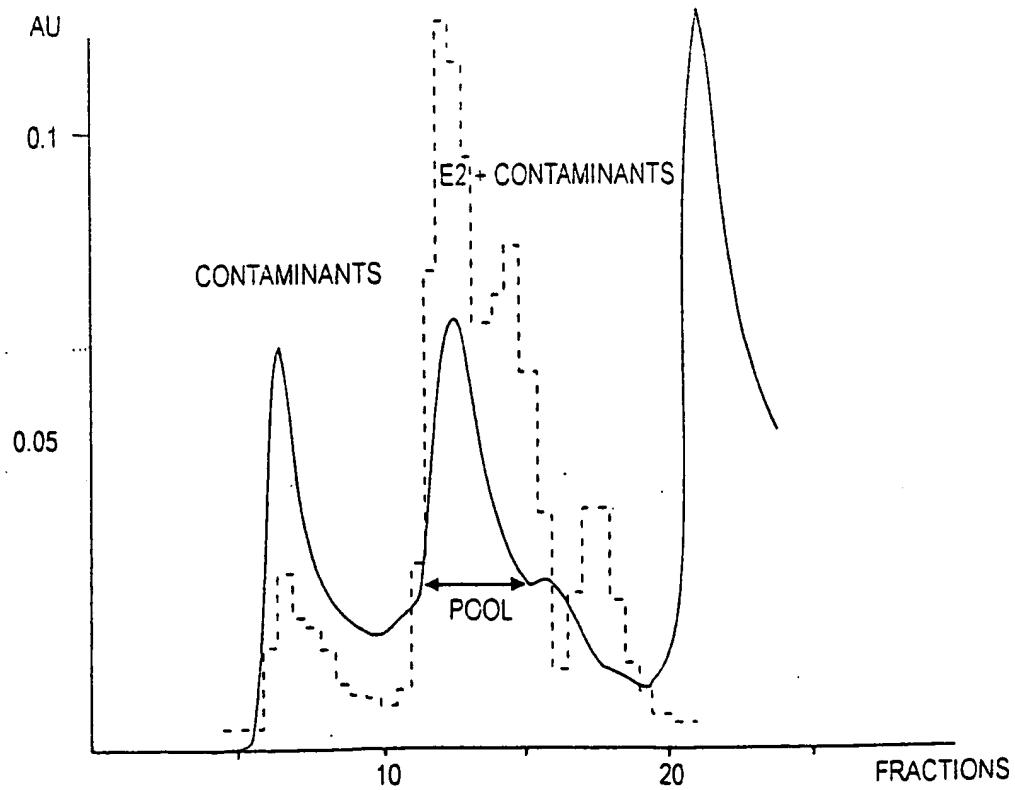


Fig. 31B

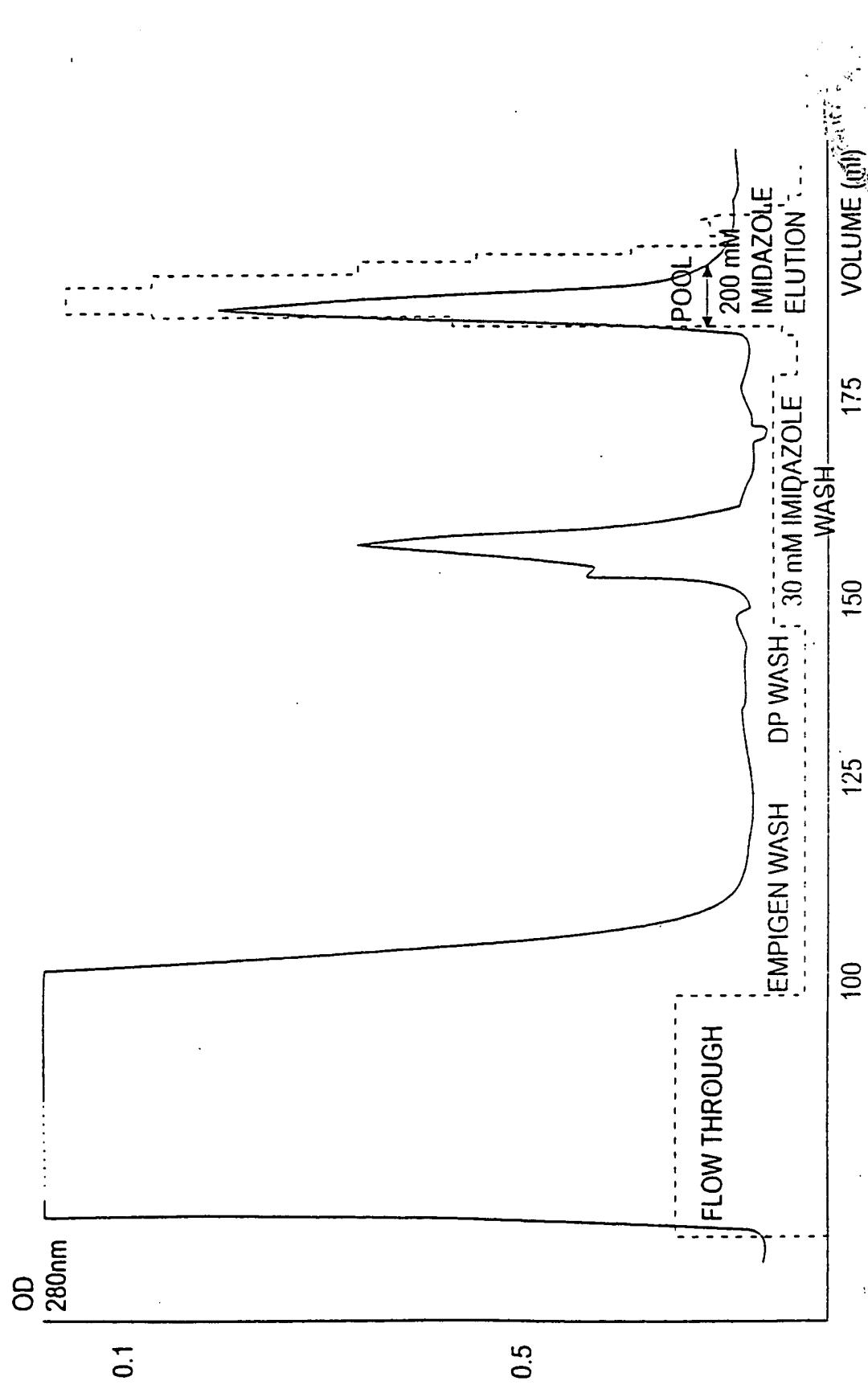
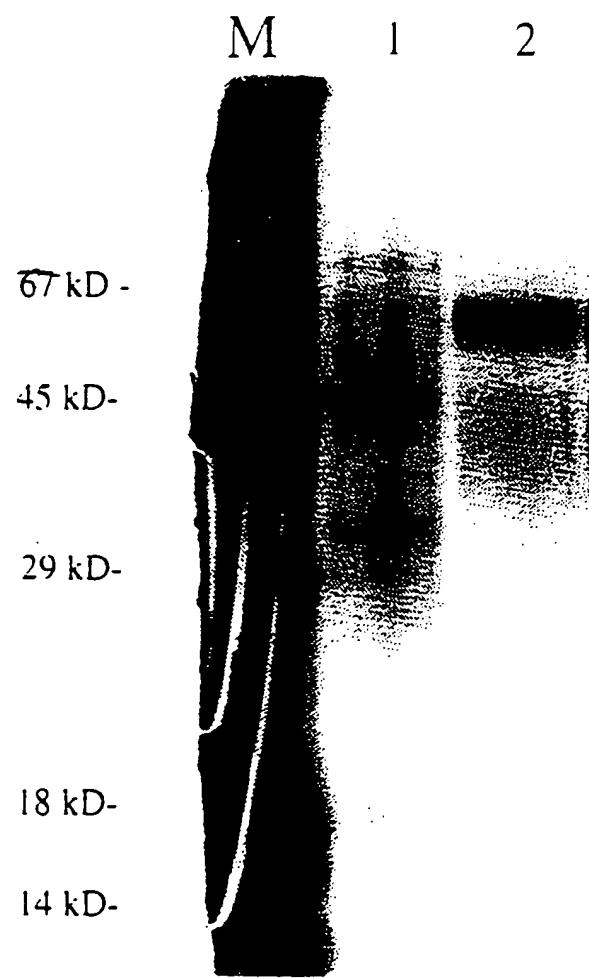


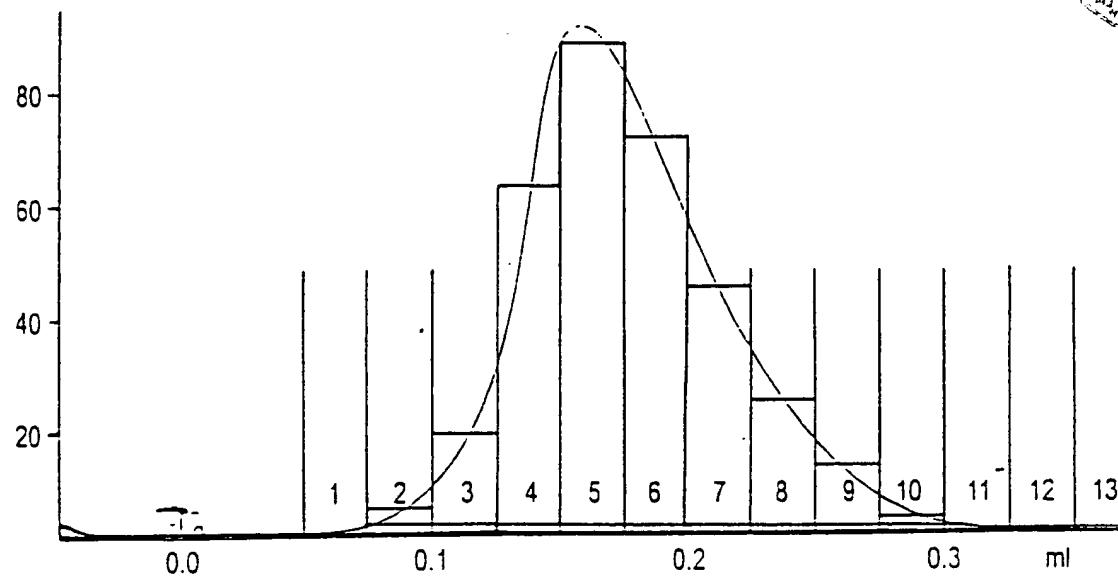
Fig. 32

## SILVER STAIN OF PURIFIED E2



1. 30 mM IMIDAZOLE WASH Ni-IMAC
2. 0.5  $\mu$ g E2

Fig.33



No.	Ret. (ml)	Peak start (ml)	Peak end (ml)	Dur (ml)	Area (ml*mAU)	Height (mAU)
1	-0.45	-0.46	-0.43	0.04	0.0976	4.579
2	1.55	0.75	3.26	2.51	796.4167	889.377
3	3.27	3.26	3.31	0.05	0.0067	0.224
4	3.33	3.32	3.33	0.02	0.0002	0.018

Total number of detected peaks = 4

Total Area above baseline = 0.796522 ml\*AU

Total area in evaluated peaks = 0.796521 ml\*AU

Ratio peak area / total area = 0.999999

Total peak duration = 2.613583 ml

Fig. 34

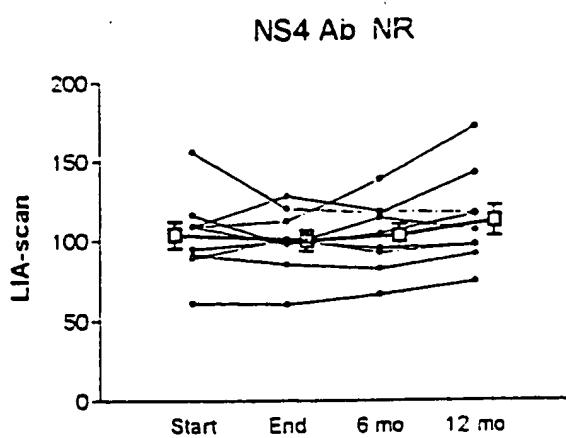


Fig. 35A-1

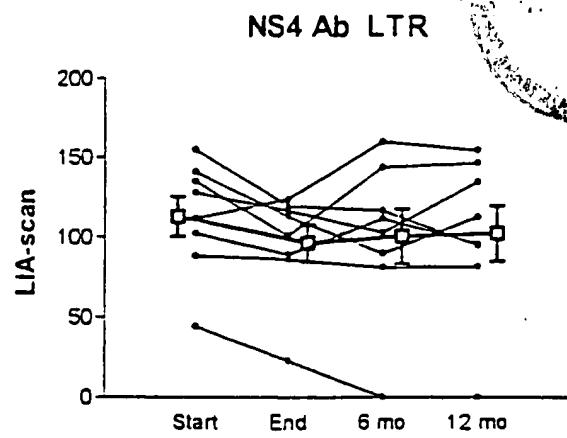


Fig. 35A-2

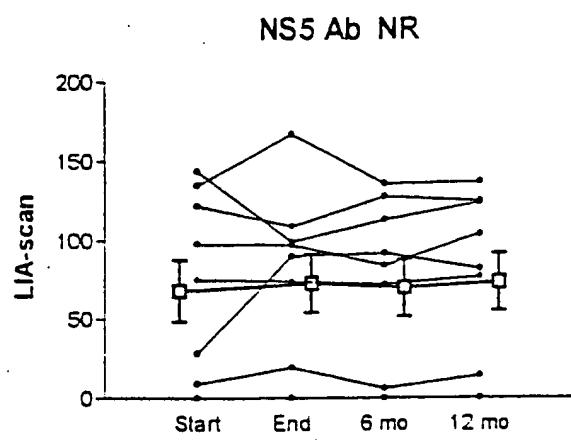


Fig. 35A-3

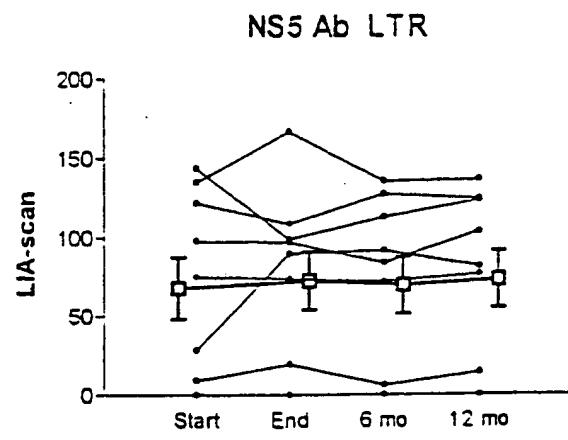


Fig. 35A-4

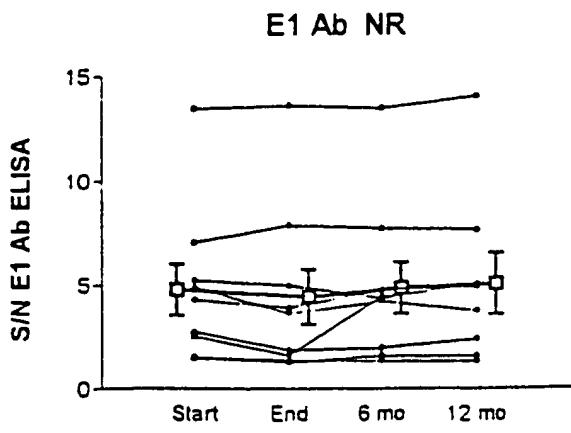


Fig. 35A-5

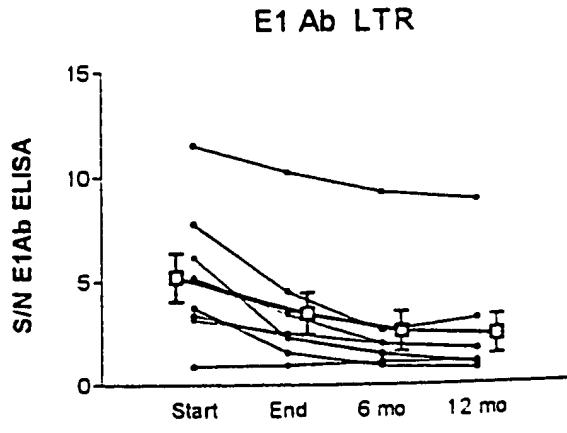
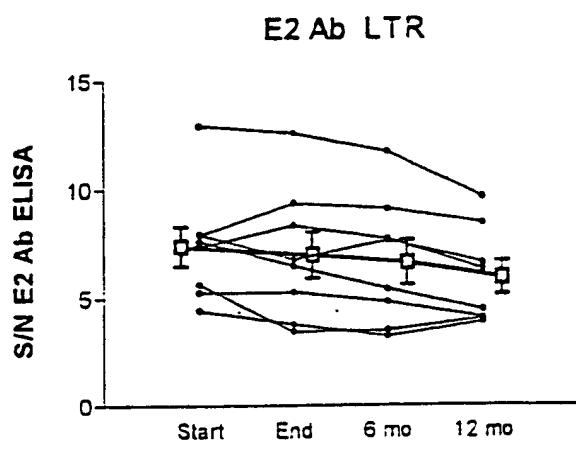
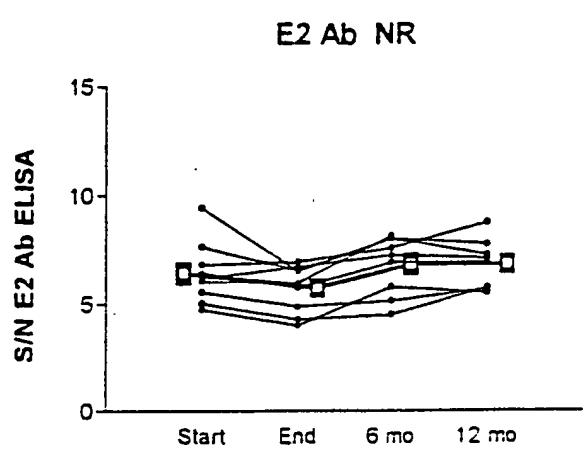


Fig. 35A-6



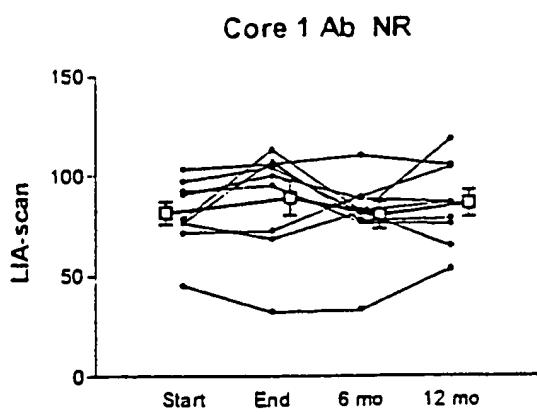


Fig. 35B-1

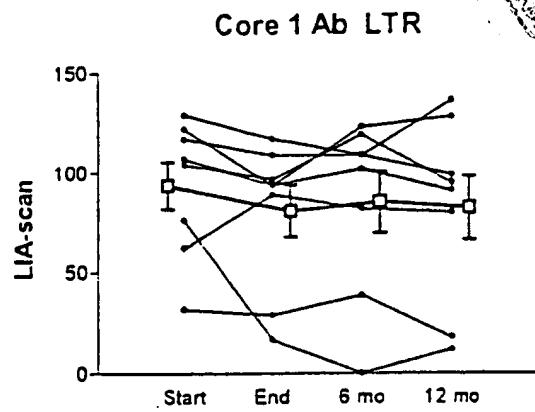


Fig. 35B-2

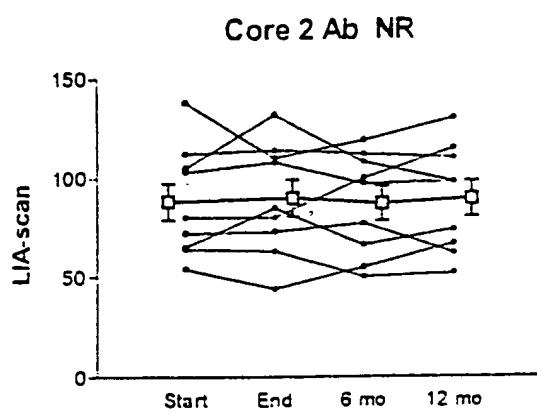


Fig. 35B-3

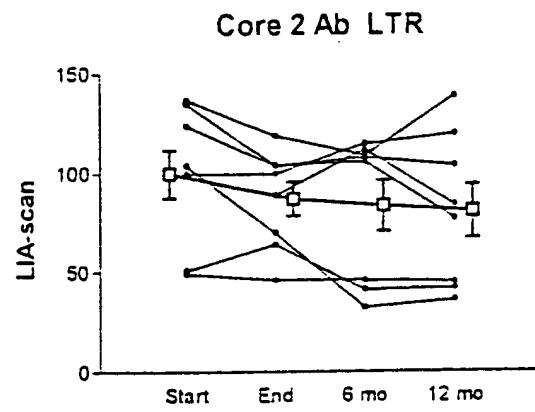


Fig. 35B-4

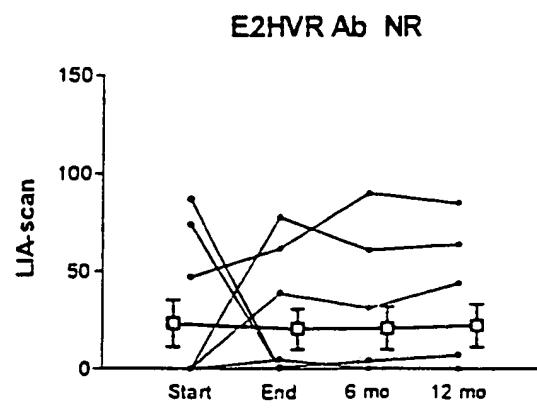


Fig. 35B-5

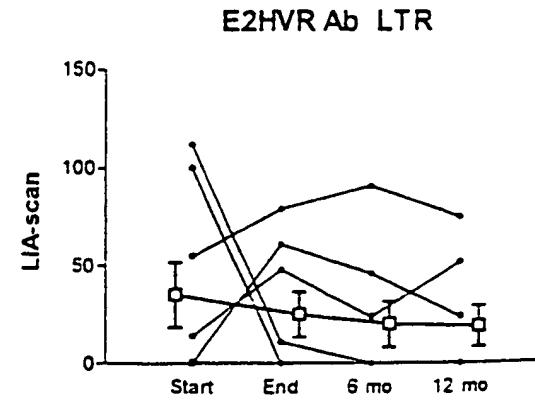


Fig. 35B-6

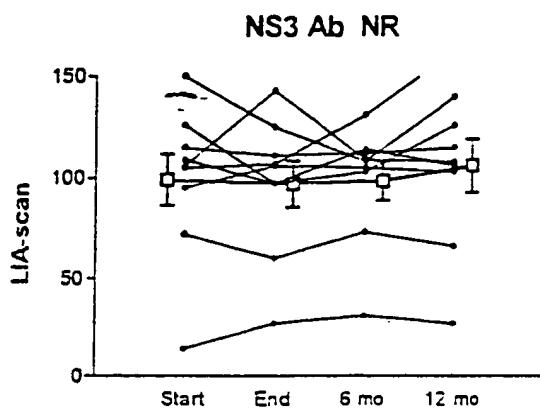


Fig. 35B-7

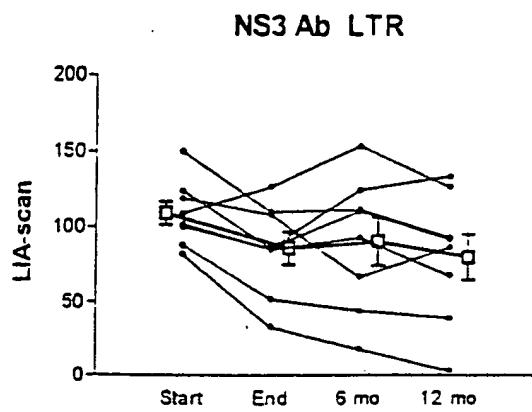


Fig. 35B-8

Fig. 36A

E1 Ab

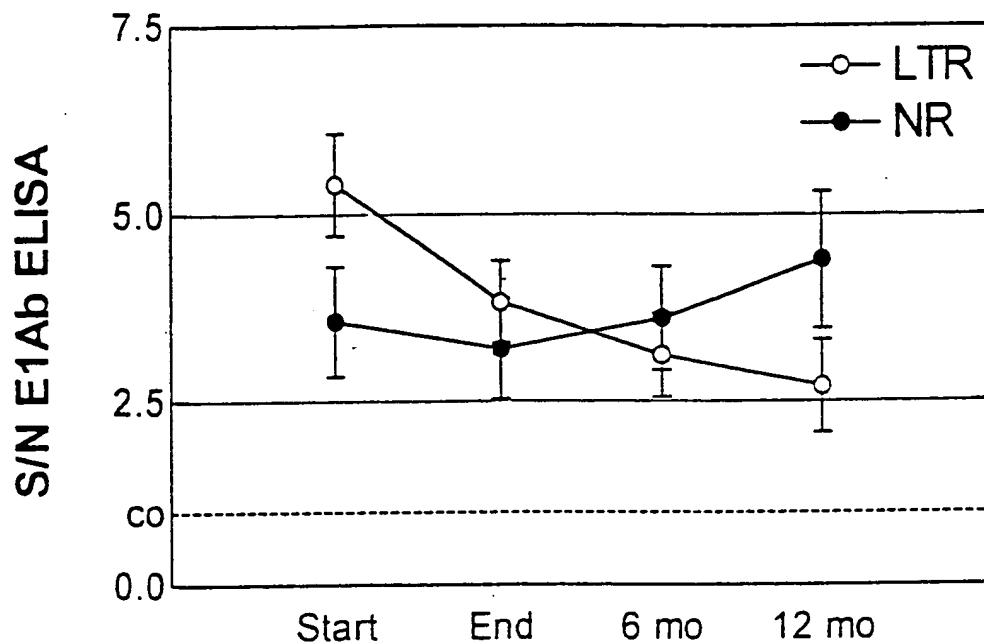


Fig. 36B

E2 Ab

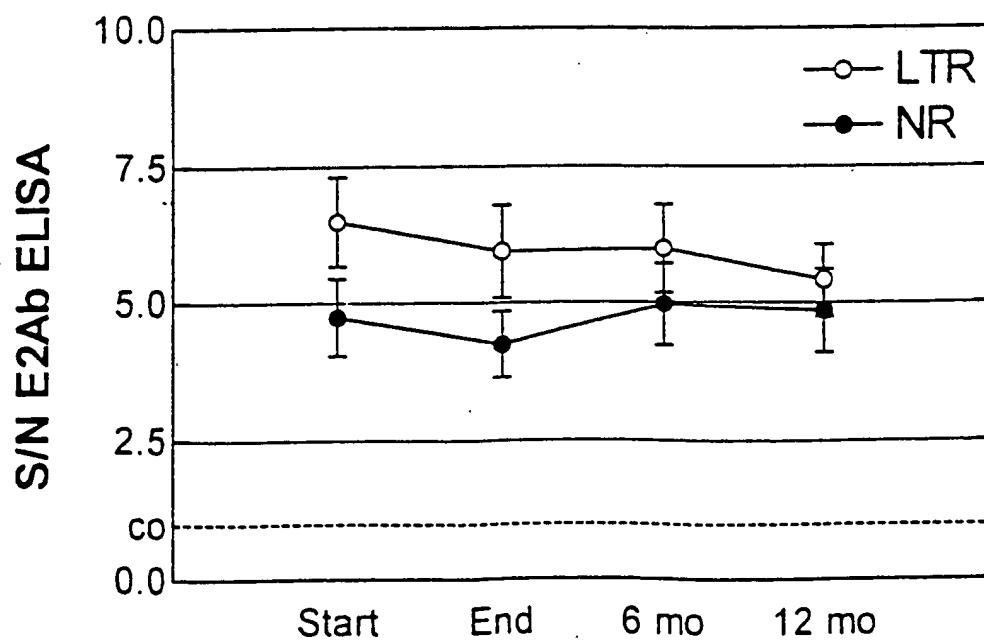


Fig. 37A  
Non Responders

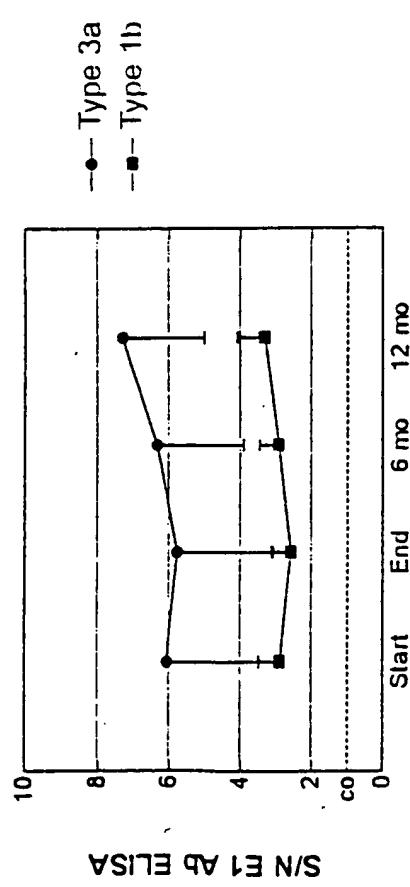


Fig. 37C  
Type 1b

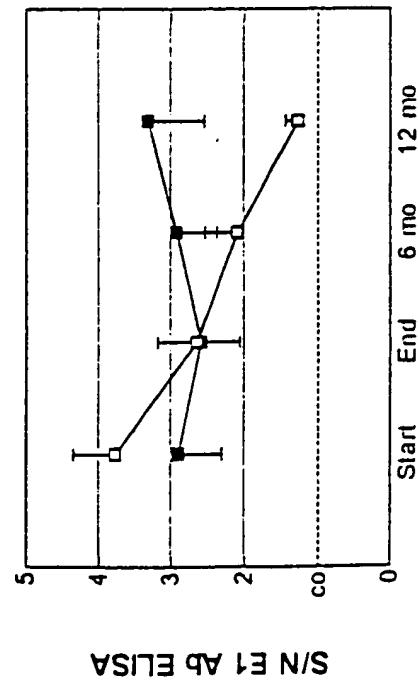


Fig. 37B  
Long Term Responders

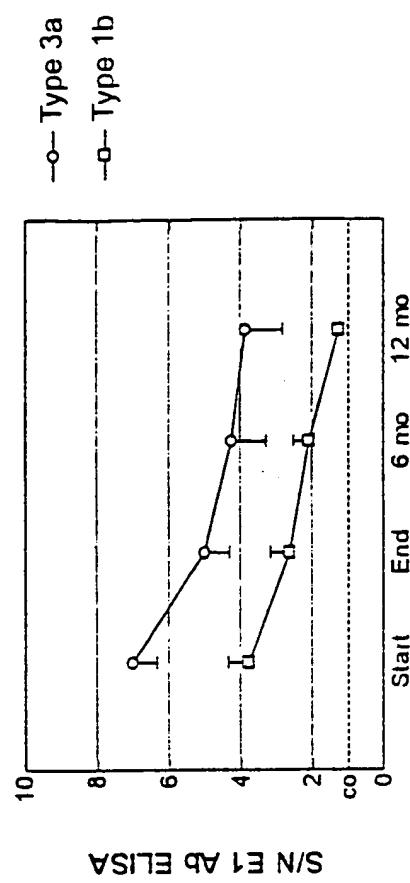


Fig. 37D  
Type 3a

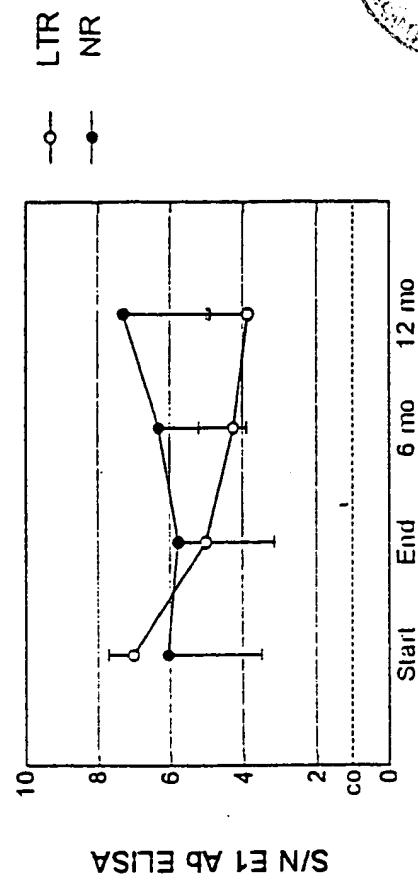
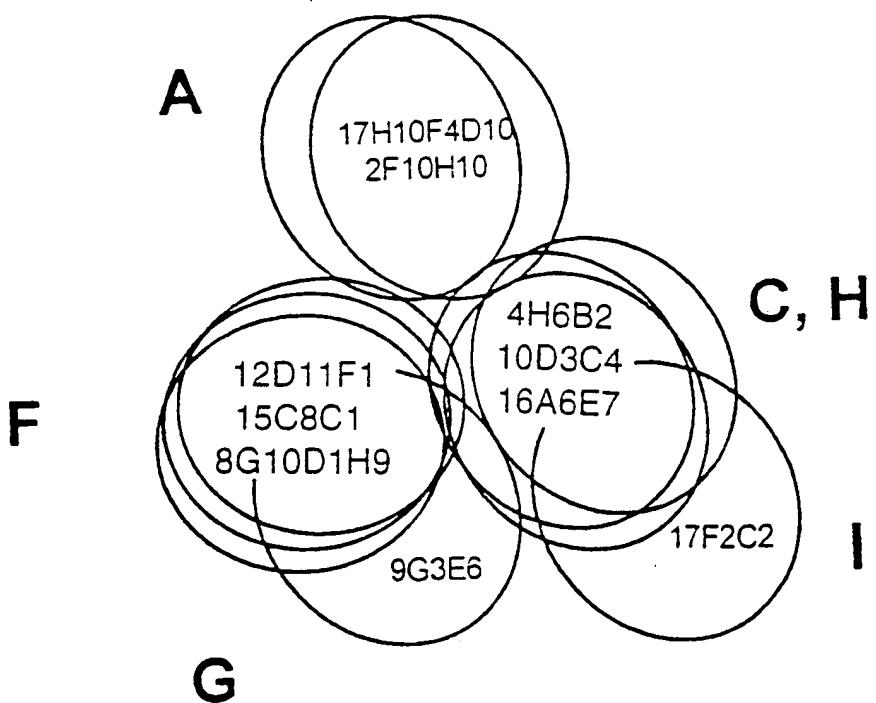
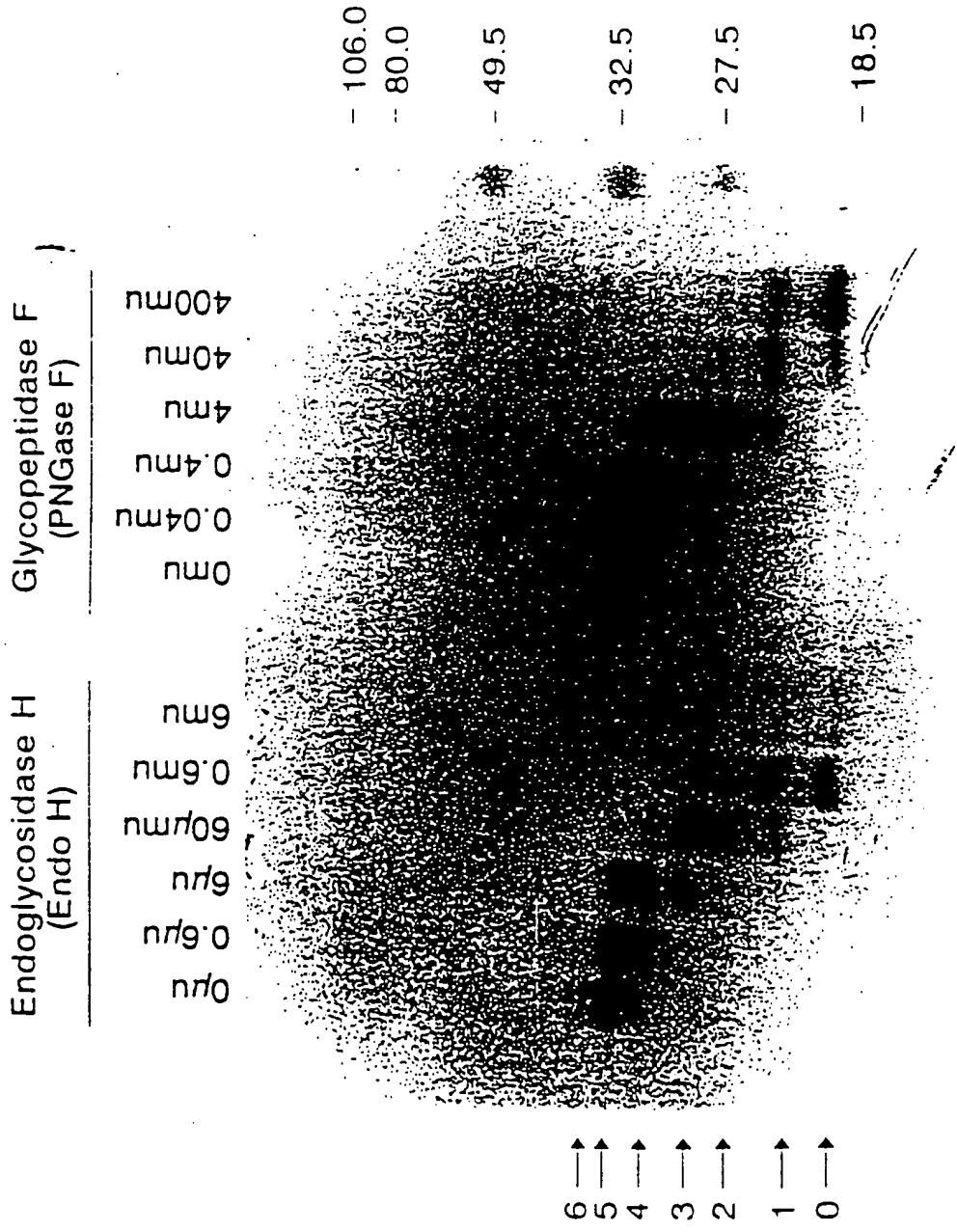


Fig. 38

Relative Map Positions of  
anti-E2 monoclonal antibodies



PARTIAL DEGLYCOSYLATION  
OF HCV E1 ENVELOPE PROTEIN



PARTIAL TREATMENT OF HCV E2\ E2s ENVELOPE PROTEINS  
BY PNGase F

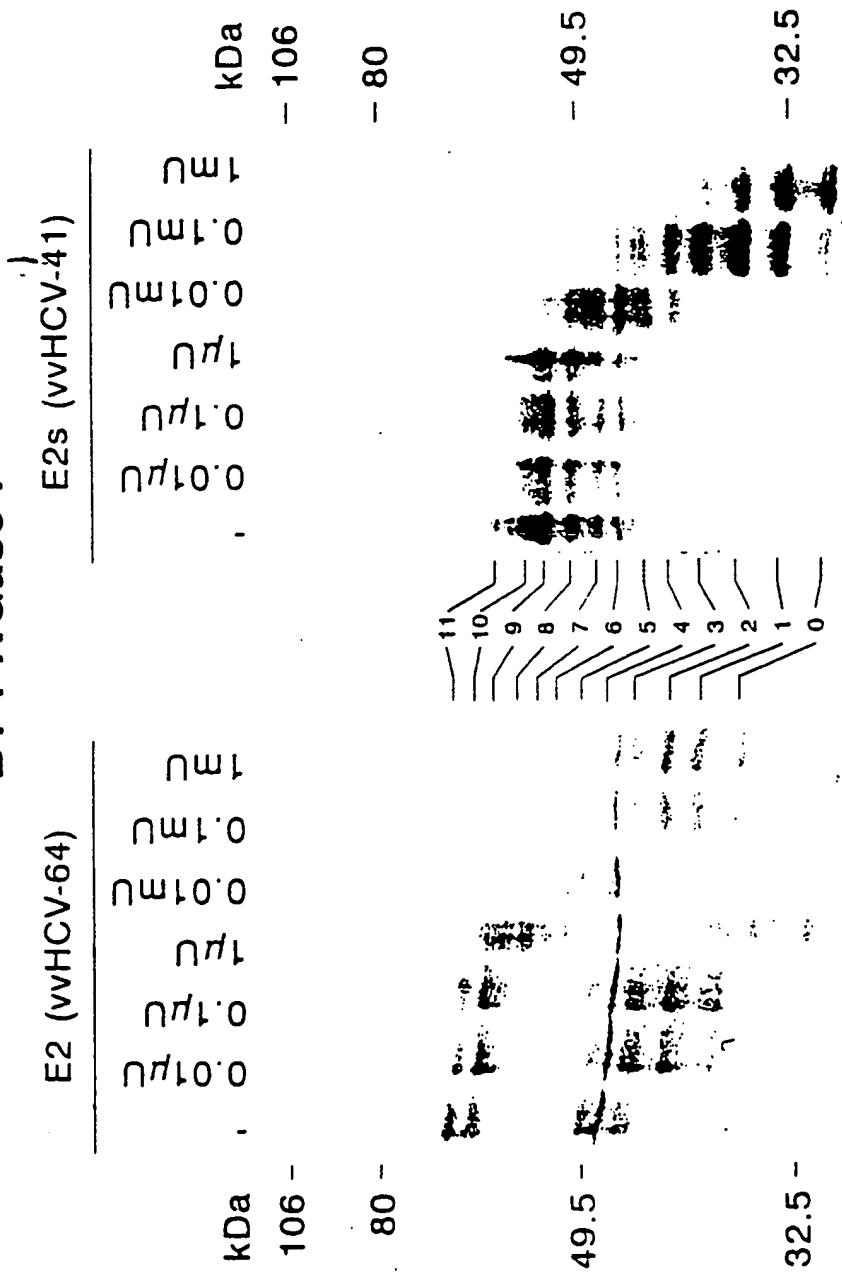


Fig. 40

**Fig. 4.1 *In Vitro* Mutagenesis of HCV E1 glycoprotein**

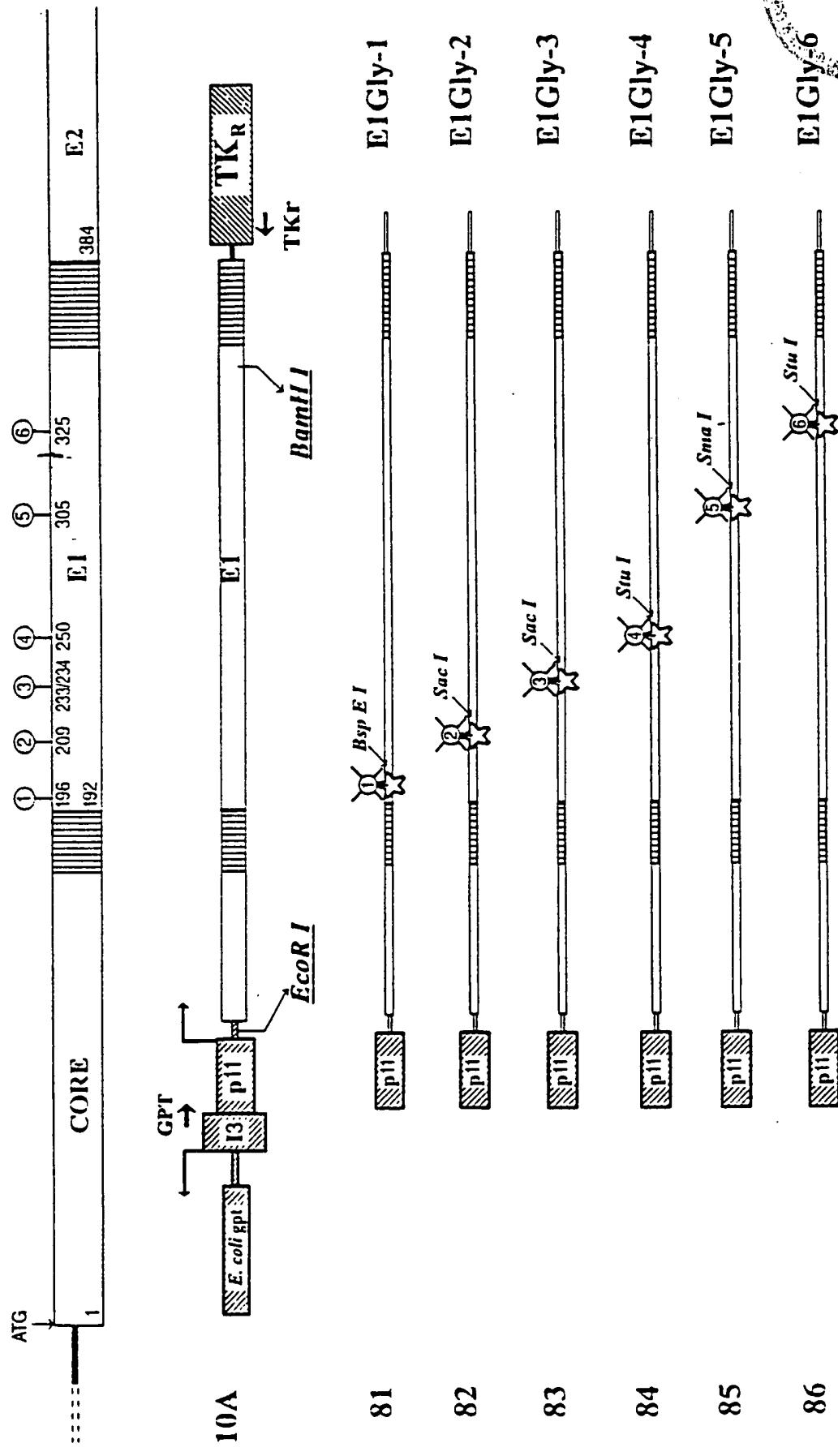
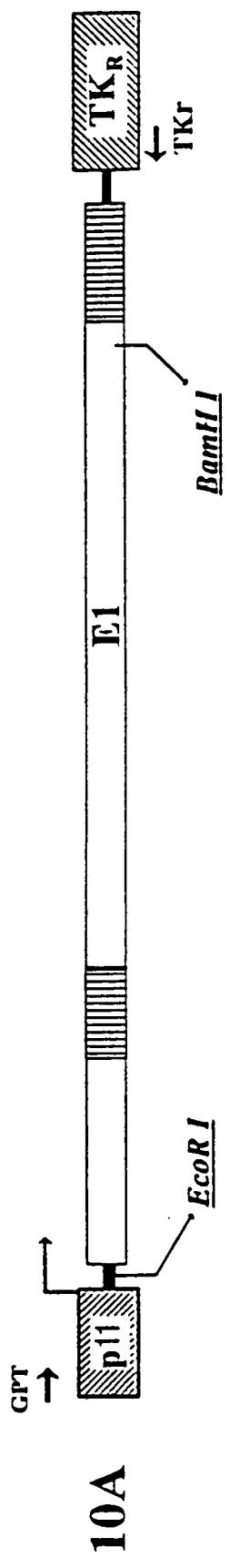
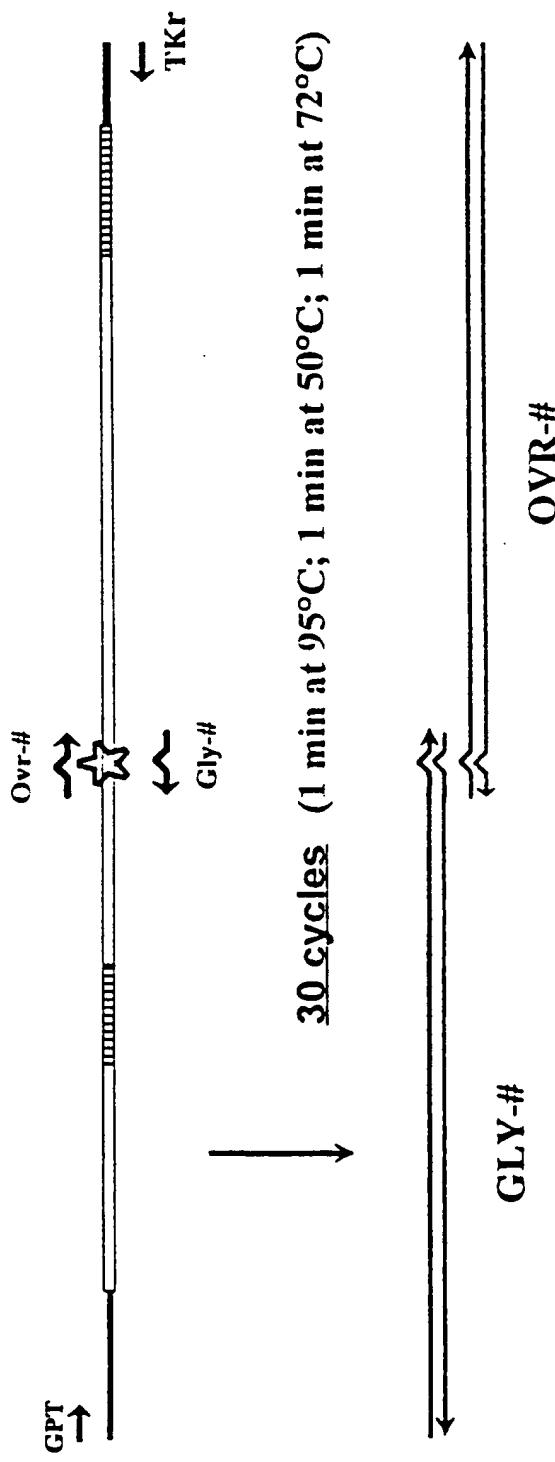


Fig. 42A *In Vitro* Mutagenesis of HCV E1 glycoprotein

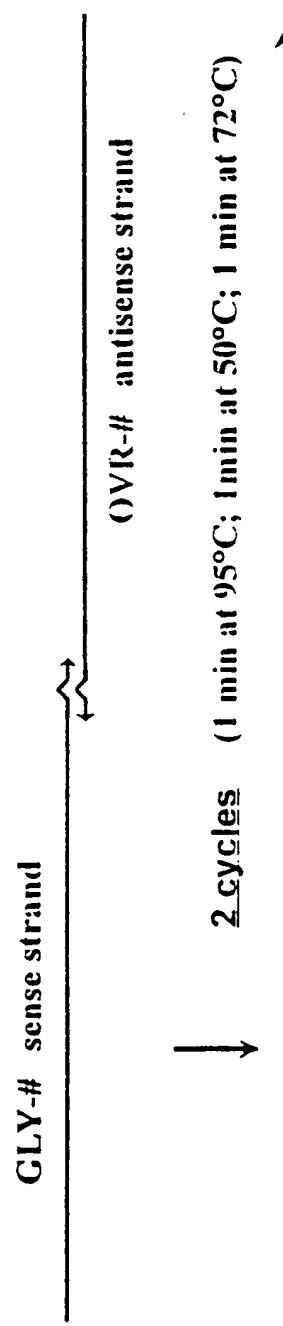


1. First step of PCR amplification (Gly-# and Ovr-# primers)



## 2. Overlap extension and nested PCR

### a. Overlap extension



### b. Nested PCR amplification (GPT-2 and TKr-2 primers)

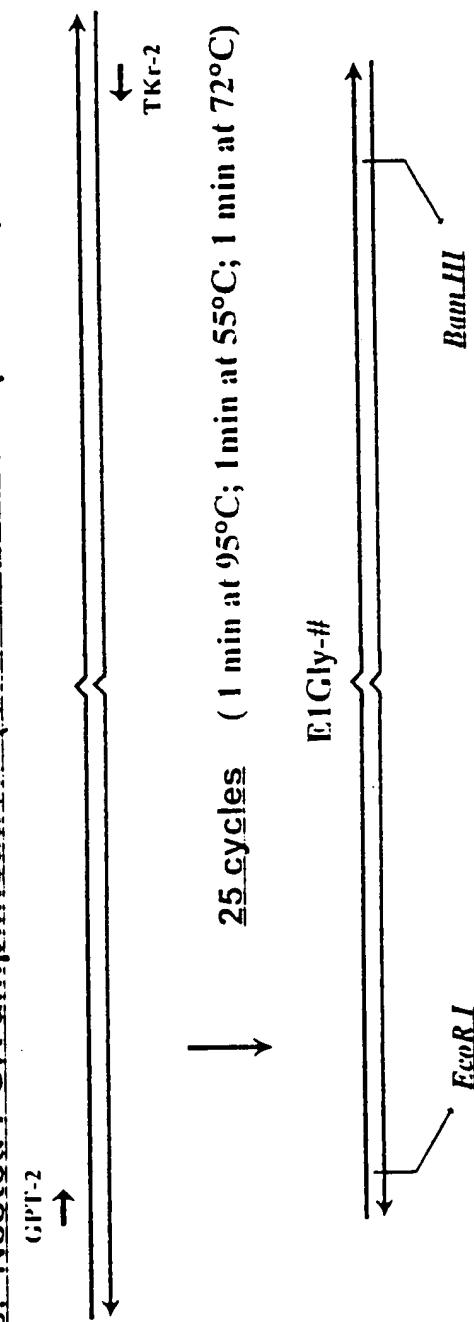
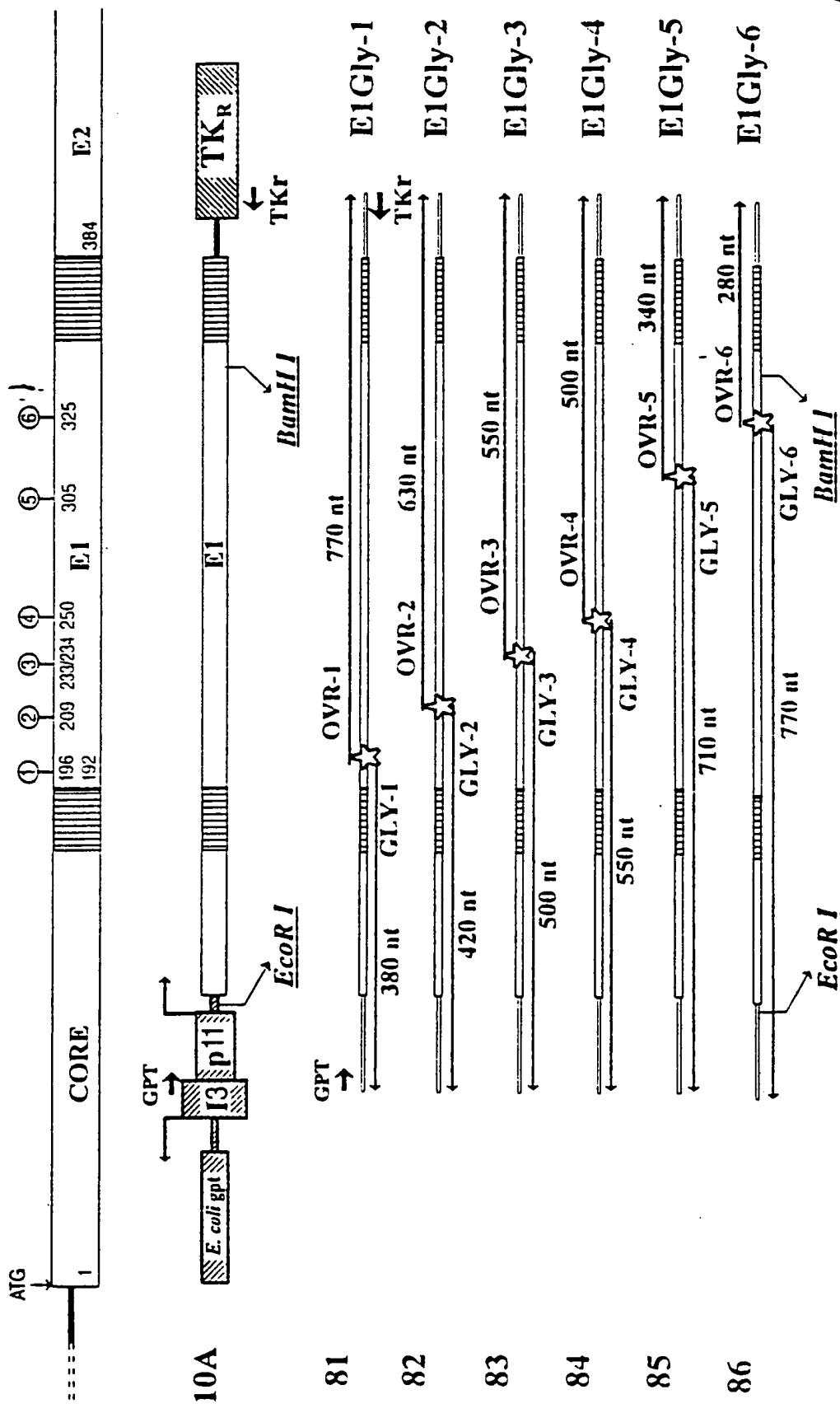


Fig. 42B

Fig. 43 *In Vitro* Mutagenesis of HCV E1 glycoprotein



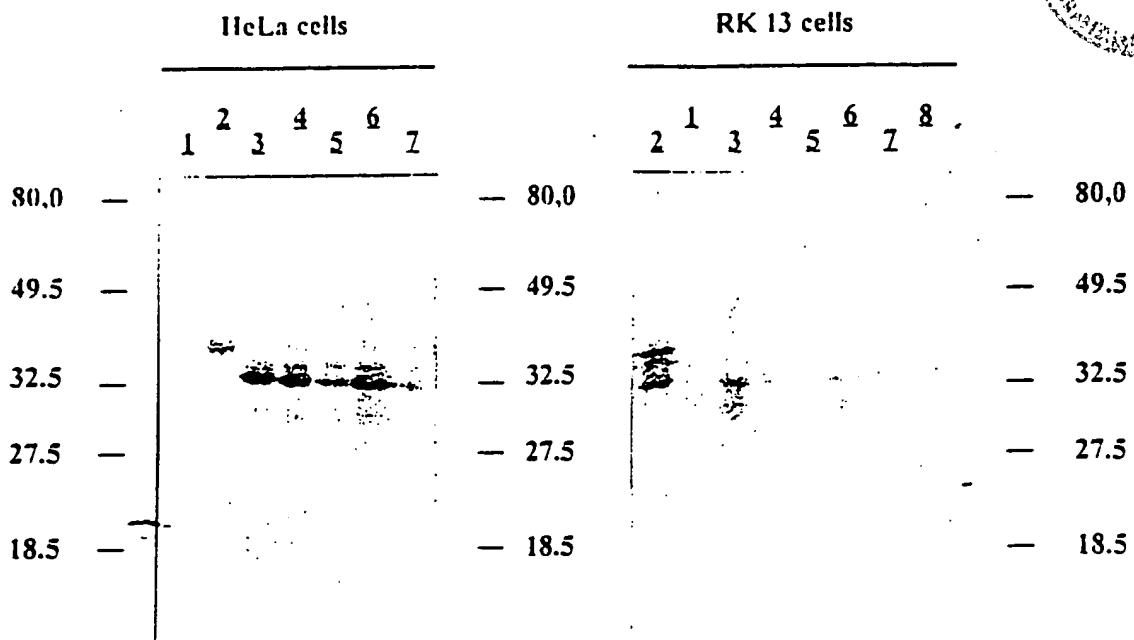


Fig. 44A

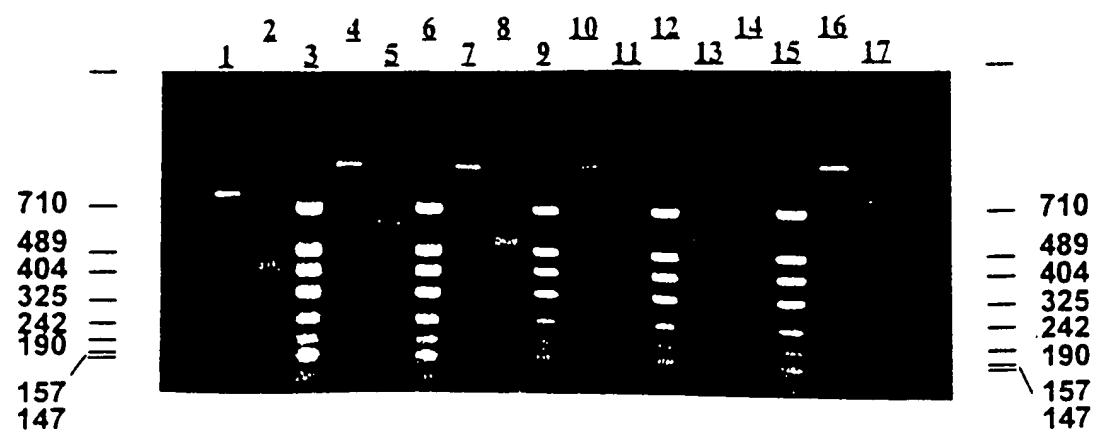


Fig. 44B

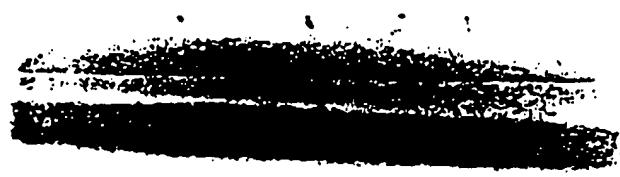


Fig. 45

KDall 9 67 43 29 18

| | | | |



Fig. 46